



MAJORITY ATGXXGGCGATGCTTCCCTCTCTTTGAGCCCAAGGCCGGTCTCCTGGTGACGGGCACCTGGCCT

DNAPTAQ ...AG..G.....G.....G.....70
DNAPTFLC..G.....67
DNAPTTH ...GA.....G.....A.....70

MAJORITY ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCACCOCGGGGGAACCGGTGCAGGGGTCTACGGCTT

DNAPTAQCA.....G.....140
DNAPTFLT.....C.....C..T.....137
DNAPTTHG.....140

MAJORITY CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGACXXGCCGGTGTCGTGGTCTTTGACGCCAAG

DNAPTAQC.....A.....207
DNAPTFLA.....GT..T.....204
DNAPTTHT..AA..C..CT.....280

MAJORITY GCCCCCTCTTCGCCACGAGGCCTACGAGGCCTACAGGGGGCCGGGCCCCACCCCGGAGGACTTTC

DNAPTAQG..GG.....G.....277
DNAPTFL274
DNAPTTHGA.....G.....C.....280

MAJORITY CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCTTGCGCGCCTCGAGGTCCCCGGCTA

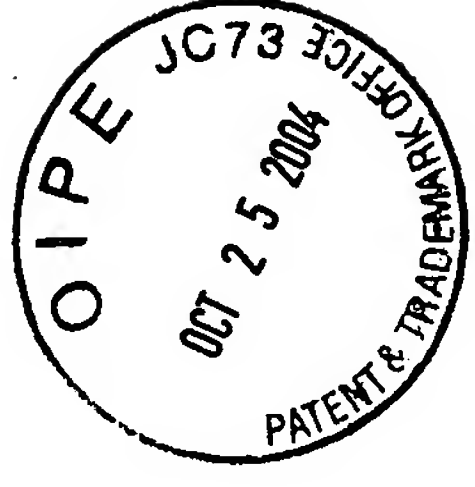
DNAPTAQA.....G.....G.....347
DNAPTFLG.....T.....A..C.....T..G..G.....T..344
DNAPTTH350

FIG. 1A

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| | | |
|----------|--|-----|
| MAJORITY | CGAGGGGACGACGTXCTGGCCACCCTGGCCAAGAGCGGAAAGGAGGGGTACGAGGTGCGCATCCTC | |
| DNAPTAQ |C.....G.....C.....C..... | 417 |
| DNAPTFL | T.....G.....CG..... | 414 |
| DNAPTTH |T..C..... | 420 |
| MAJORITY | ACCGCCGACCGGACCTCTACGACTCCTTTCCGACCGCATCGCCGTCTCCACCCCGAGGGGTACCTCA | |
| DNAPTAQ |AAA.....T.....CA..... | 487 |
| DNAPTFL | ..T.....G..G.....A.....T.....G.. | 484 |
| DNAPTTH |A..G.C.....G.....CC..... | 490 |
| MAJORITY | TCACCCCGCGGTGGCTTTGGGAGAAGTACGGCCTGAGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC | |
| DNAPTAQ |C.....A.....C..C.....CC.....A.. | 557 |
| DNAPTFL |AC.....C.C..... | 554 |
| DNAPTTH |A.....C.....C.....T..C.....C.T | 560 |
| MAJORITY | GGGGGACCCCTCCGACAACCTCCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCXGAAGCTCCTCXAG | |
| DNAPTAQ | C.....GAG.....T.....G..GAG.....T..GG.. | 627 |
| DNAPTFL |G..T..A.....G.....A..G....A..CGC | 624 |
| DNAPTTH |TC.....A.. | 630 |
| MAJORITY | GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCCGC...XTCCGGGAGAAGA | |
| DNAPTAQ |GC.....C.....A..... | 694 |
| DNAPTFL |T..C..C.....A.....T....T.G.....C | 691 |
| DNAPTTH |A.....A....A.AAAA.G..... | 700 |

FIG. 1B



MAJORITY TCCAGGCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCAGGTGCGCACCGACCTGCCCCCTGGA

DNAPTAQC..T....A.....C..GG..A..... 764
DNAPTFLGGG.....G.C....GCC..T...C..A....T.....A...T..... 761
DNAPTTH ..A.....C.....A.....C.G.....T.....C.....C..... 770

MAJORITY GGTGGACTTCGCCAAGXGGCGGGAGGCCCGACCGGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT

DNAPTAQAA.....A.....A.....A.....T.....T..... 834
DNAPTFLGG.G.C.C..CACA...A...T.....T..GC....T...T.....C..T..... 831
DNAPTTHC.....C..G.....C.....C.....C.....C.....C..... 840

MAJORITY GGCAGCCTCCTCCACGAGTTCGGCCTCCTGGAGGGCCCCAAGGCCCTGGAGGAGGCCCTGGCCCCCGC

DNAPTAQT.....AA..... 904
DNAPTFL ..A.....G.....G..G....GGCA.....T..... 901
DNAPTTHC.....C....GCCC..... 910

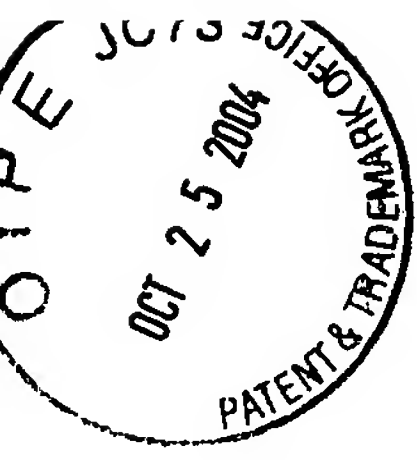
MAJORITY CGGAAGGGCCTTCGTGGGCTTTGTCTTCCCGCCCCGAGCCCCATGTGGGCCGAGCTTCTGGCCCCCTGGC

DNAPTAQG.....AAG.....T..... 974
DNAPTFLT..TT.....TC.T.....T..... 971
DNAPTTHC.....C.....G.....AAA..... 980

MAJORITY CGCCGCCAGGGAGGGCCGGGTCCACCGGGCACCGACCCCTTTAXGGGCCCTXAGGGACCTXAAGGAGGTG

DNAPTAQG.....C..C..G..T.A..AA.C...C.....G.....C. 1044
DNAPTFL T.GG..GT.....G..CC...T.....A.....C...G.....G.....T.....G..... 1041
DNAPTTHTG.....C.....G.....G.....G..A.A.....C.....C..... 1050

FIG. 1C



MAJORITY CGGGXCTCCTCGCCAAGGACCTGGCCGTTTGGCCCTGAGGGAGGCCCTXGACCTCXTGCCCGGGGACG

DNAPTAQG..T.....A.....AG.....C.....A.....T.G.....CC.....C..... 1114
DNAPTFLAA.....G.....G.....C.....T.C.....A.A..... 1111
DNAPTTHC.....C.....TC.....G.A.....G..... 1120

MAJORITY ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCCCGAGGGGTGGCCCGGCTACGG

DNAPTAQT.....T..... 1184
DNAPTFLG.....T.....T.....T..... 1181
DNAPTTHG.....G..... 1190

MAJORITY GGGGGAGTGGACGGAGGAXGCGGGGGAGCGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG

DNAPTAQ C.....G.....GC.....T.....GCC.....GTG..G. 1254
DNAPTFLT.....A.....GG.....C.C.....A..C...AAA.... 1260
DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA.. 1260

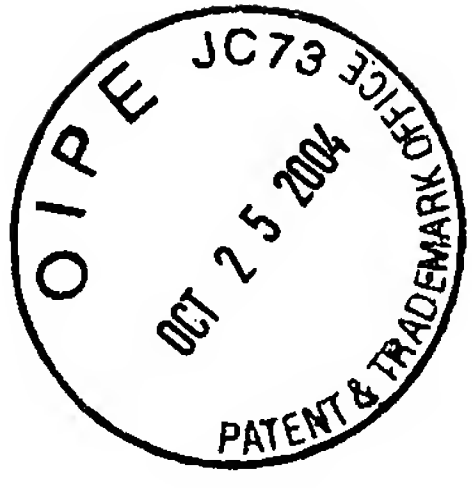
MAJORITY CGCCTTGAGGGGAGGAGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCTTTCCCGGGTCCIGG

DNAPTAQ A.G.....G.....G.....GCT..... 1324
DNAPTFLA..A..AC.C..G.....G.....GT... 1321
DNAPTTHC.....A.....C.....C..... 1330

MAJORITY CCCACATGGAGGCCACGGGGGTXC GGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA

DNAPTAQG..C.....T...AG....T.G.....C.. 1394
DNAPTFLGG.....C.....C.....A..C 1391
DNAPTTHC.....A.....T.....C.T..... 1400

FIG. 1D



MAJORITY GGAGATCCGCCCTCGAGGAGGAGGTCTTCCGCCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGGGAC

DNAPTAQGC.....CC..... 1464
DNAPTFLG.G....AG..G.....C... 1461
DNAPTTHT.....G..... 1470

MAJORITY CAGCTGGAAAGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC

DNAPTAQC.....A.....C..... 1534
DNAPTFLGC.....G.C..G..T.....G..G..A.. 1531
DNAPTTHTA.....T.G..G.....C.A.....A..... 1540

MAJORITY GCTCCACAGCGCCGCGTGCTGGAGGCCCTXCGXGAGGCCACCCCATCGTGGAGAAGATCCTGCAGTA

DNAPTAQC.....C..... 1604
DNAPTFLT.....G.A.....CCGC..... 1601
DNAPTTHG.....A.G.....C...C.. 1610

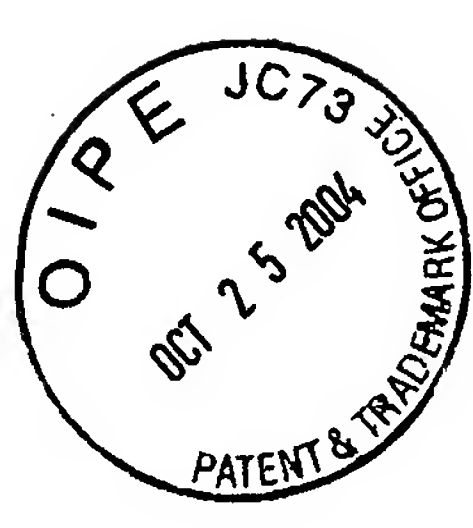
MAJORITY CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCCXGXCCCTCGTCCACCCAGGACGGGC

DNAPTAQG....G.....T....T....G.A...A..... 1674
DNAPTFLA.....A.....C.C...G.....A...C... 1671
DNAPTTHG.G.....AAG.....G..... 1680

MAJORITY CGCCTCCACACCCGCTTCAACCAGACGGCCACGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC

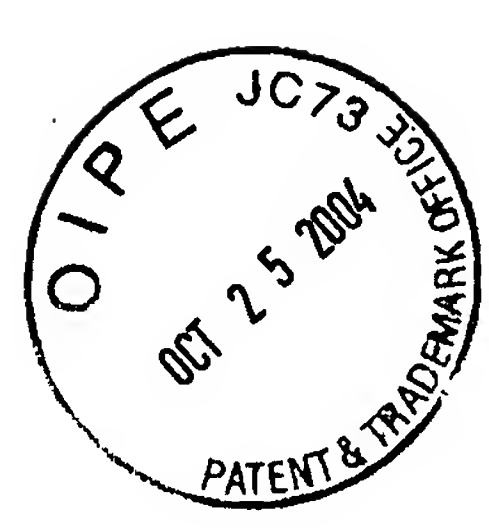
DNAPTAQA.....A.....T.....C.. 1744
DNAPTFLG.....C.....TCC..... 1741
DNAPTTHG..... 1750

FIG. 1E



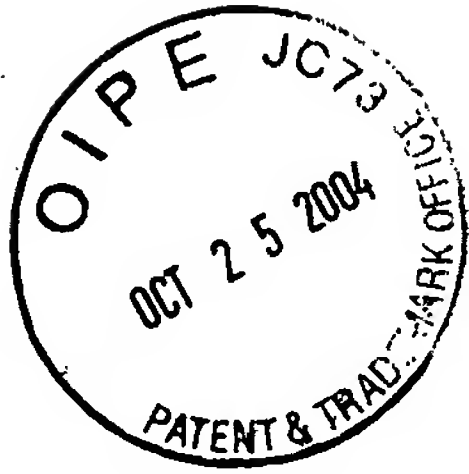
| | | | | | | | | | | | |
|----------|---|--|--|--|--|--|--|--|--|--|------|
| MAJORITY | | AGAACATCCCCGTCGCCACCCXCTGGGCCAGAGGATCCGCCGGCCCTTCGTGGCCGAGGAGGGXTGGGT | | | | | | | | | |
| DNAPTAQ | | | | | | | | | | | 1814 |
| DNAPTFL | | | | | | | | | | | 1811 |
| DNAPTTH | | | | | | | | | | | 1820 |
| MAJORITY | | GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTCTGGCCACCTCTCCGGGGACGAGAACCTG | | | | | | | | | |
| DNAPTAQ | A | | | | | | | | | | 1884 |
| DNAPTFL | C | | | | | | | | | | 1881 |
| DNAPTTH | | | | | | | | | | | 1890 |
| MAJORITY | | ATCCGGGTCTTCCAGGAGGGGAGGACATCCACACCCAGACCCGACCTGGATGTTCCGGCGTCCCCCCGG | | | | | | | | | |
| DNAPTAQ | | | | | | | | | | | 1954 |
| DNAPTFL | | | | | | | | | | | 1951 |
| DNAPTTH | | | | | | | | | | | 1960 |
| MAJORITY | | AGGCCGTGGACCCCTGATGCGCCGGCGGCAAGACCATCAACTTCGGGGTCTCTACGGCATGTCCGC | | | | | | | | | |
| DNAPTAQ | | | | | | | | | | | 2024 |
| DNAPTFL | A | | | | | | | | | | 2021 |
| DNAPTTH | | | | | | | | | | | 2030 |
| MAJORITY | | CCACCGCCTCTCCAGGAGCTTGCCATCCCCCTACGAGGAGCGGTGGCCCTTCATTGAGCGCTACTTCCAG | | | | | | | | | |
| DNAPTAQ | | | | | | | | | | | 2094 |
| DNAPTFL | | | | | | | | | | | 2091 |
| DNAPTTH | | | | | | | | | | | 2100 |

FIG. 1F



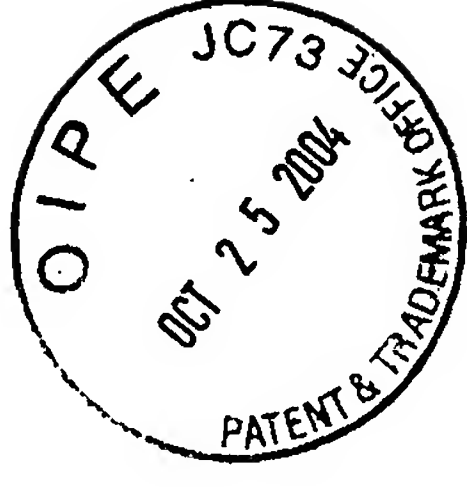
| | | | |
|----------|--|---|------|
| MAJORITY | | AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGCGAGGCGGGGTACGTGGAGA | |
| DNAPTAQ | | | 2164 |
| DNAPTFL | ...A..... | ...GG...C...C.CC...T..... | 2161 |
| DNAPTTH | | ...A..A.....G...A.....C.....A. | 2170 |
| MAJORITY | | CCCTCTTCGGCCGCGGCTACGTGCCCGACCTCAACGCCCGGGTGAAGAGCGTGCGGGAGGCGGCGGA | |
| DNAPTAQ | | ...C.....A...AG.G.....C... | 2234 |
| DNAPTFL | | ...T.....C..... | 2231 |
| DNAPTTH | ...AA.AA..... | ...CA.....C..... | 2240 |
| MAJORITY | | GCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGACCTCATGAAGCTGGCCATGGTGAAGCTC | |
| DNAPTAQ | |T..... | 2304 |
| DNAPTFL | | ...G.....CG...T | 2301 |
| DNAPTTH | | ...C..... | 2310 |
| MAJORITY | | TTCCCCCGGCTXCAGGAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCCCTCGAGGCC | |
| DNAPTAQ | ...A...GG..... | ...T..... | 2374 |
| DNAPTFL | ...T...C...G...TT.G...G..... | ...G..... | 2371 |
| DNAPTTH | ...C..C.G...G...C.C.....C.....G..... | ...CC...G..... | 2380 |
| MAJORITY | | CCAAAGAGCGGGGAGGXGGTGGCCGCTTTGGCCAAGGAGGTTCATGGAGGGGTCTATCCCCCTGGCCGT | |
| DNAPTAQ | .A.....A.....CC.....CGGC..... | ...G..... | 2444 |
| DNAPTFL | ...G..C.....AG...A..... | ...GG.....CAG... | 2441 |
| DNAPTTH | ..C...C.....C...A.....G.....C.....AA..C.....C..... | ...C..... | 2450 |

FIG. 1G



| | | |
|----------|---|------|
| MAJORITY | GCCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG | |
| DNAPTAQ |A.....GA | 2499 |
| DNAPTFL |CC..... | 2496 |
| DNAPTTH |T.....GT... | 2505 |

FIG. 1H



MAJORITY MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVPQAVYGFAKSLLKALKEDG·DAVXVVVFDK

| | | |
|---------|---------------------|----|
| TAQ PRO | RG.....H.....I..... | 69 |
| TFL PRO |V.....V..... | 68 |
| TTH PRO | E.....YK..F..... | 70 |

MAJORITY APSFRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL

| | | |
|---------|--------------------------|-----|
| TAQ PRO |GG.....A.....S..... | 139 |
| TFL PRO |V.....F.....R..... | 138 |
| TTH PRO |FT..... | 140 |

MAJORITY TADRDLYQLLSDRIAHLPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPDNLPGVKGIGEXTAKLLX

| | | |
|---------|--|-----|
| TAQ PRO |K.....H.....D..A.....T..E.....R...E | 209 |
| TFL PRO |E...I.....Y.....A.....I.....QR..IR | 208 |
| TTH PRO |V...V.....H...E.....F...V.....L...K | 210 |

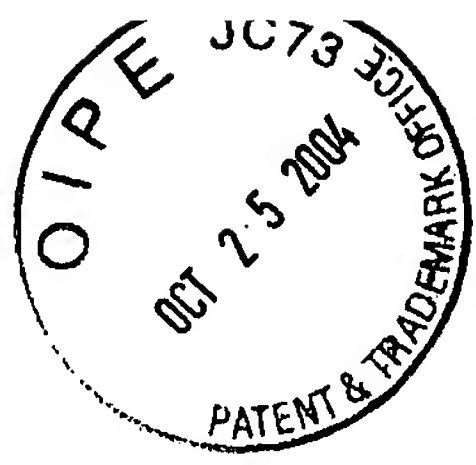
MAJORITY EWGSLENLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDREGLRAFLELRF

| | | |
|---------|---|-----|
| TAQ PRO |A.....L...AI...L...D..K..WD.AK.....K.....R..... | 278 |
| TFL PRO |FQH..Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL..... | 277 |
| TTH PRO |ENV.....K..L...R..LE..R.....L.QG..... | 280 |

MAJORITY GSLLHEFGLLEXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEELLALAAARXGRVHRAXDPLXGLRDLKEV

| | | |
|---------|---|-----|
| TAQ PRO |S.....K.....D.....PE.YKA.....A | 348 |
| TFL PRO |G...A.....L..SF.....G.WE..L...Q...R.....G. | 347 |
| TTH PRO |A.AP.....K.....C.D.....A...A..K..... | 350 |

FIG. 2A



MAJORITY RGLLAKDLAVLALREGLDLXPDDPMLLAYLLDPSNTTPEGVARRYGGWETEDAGERALLSERLFXNLXX

| | | | | | | | |
|---------|-------------|----------|--------|---------|--------|----|-----|
| TAQ PRO |S..... | G.P..... | E..... | A..... | A..... | WG | 418 |
| TFL PRO |I..... | F.E..... | | A..... | QT.KE | | 417 |
| TTH PRO |S..... | V..... | | AH..... | HR..LK | | 420 |

MAJORITY RLEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLLEEVRFLAGHPFNLNSRD

| | | | | | | | |
|---------|-------------|--------|--------|-------------|--|--|-----|
| TAQ PRO |R..... | R..... | A..... | A..... | | | 488 |
| TFL PRO |K..... | E..... | R..... | EA.V.Q..... | | | 487 |
| TTH PRO |K..... | H..... | | L..... | | | 490 |

MAJORITY QLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKNITYIDPLPXLVHPRTG

| | | | | | | | |
|---------|-------|--------------|---------|--------|----------|--------|-----|
| TAQ PRO | | | | S..... | D.I..... | | 558 |
| TFL PRO | | | DR..... | | A..... | K.. | 557 |
| TTH PRO | | R..L..Q..... | | H..... | V..... | S..... | 560 |

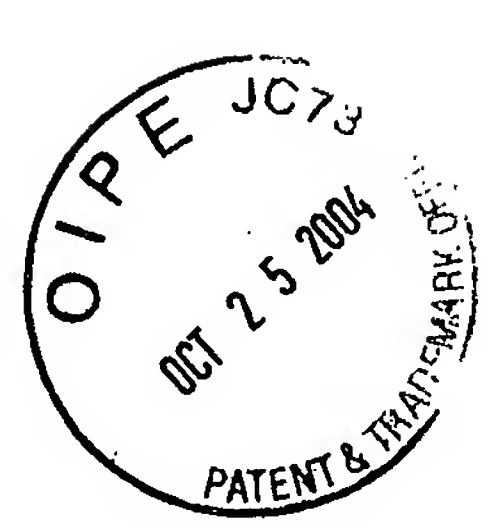
MAJORITY RLHTRFNQTATGRLLSSDPNLQNIPTVPLGQIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL

| | | | | | | | |
|---------|-------|-------|--------|-----------|--|--|-----|
| TAQ PRO | | | I..... | L..... | | | 628 |
| TFL PRO | | | | V..V..... | | | 627 |
| TTH PRO | | | | A..A..... | | | 630 |

MAJORITY IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPIYEEAVAFIERYFQ

| | | | | | | | |
|---------|-------|--------|-----------|--------|-----------|--|-----|
| TAQ PRO | | E..... | R..... | | Q..... | | 698 |
| TFL PRO | | | S..G..... | | G..S..... | | 697 |
| TTH PRO | | K..... | | V..... | | | 700 |

FIG. 2B



MAJORITY SFPKVRWIEKTL EEGRRRGYVETLFGRRRYVPDLNARVKSREAAERMAFNMPVQGTADLMKLAMVKL

| | | |
|---------|-----------------|-----|
| TAQ PRO |E..... | 768 |
| TFL PRO | .Y.....G.....R. | 767 |
| TTH PRO |K..... | 770 |

MAJORITY FPRLXEMGARMLLQVHDELVLEAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX

| | | |
|---------|---|-----|
| TAQ PRO |E.....A..R.....I..... | 833 |
| TFL PRO | ...Q.L.....D...R.....W..Q..L..... | 831 |
| TTH PRO | ...R.....L....QA...E....A..KA.....M.....G | 835 |

FIG. 2C

Genes for Wild-Type and Pol(-)DNAPTaq

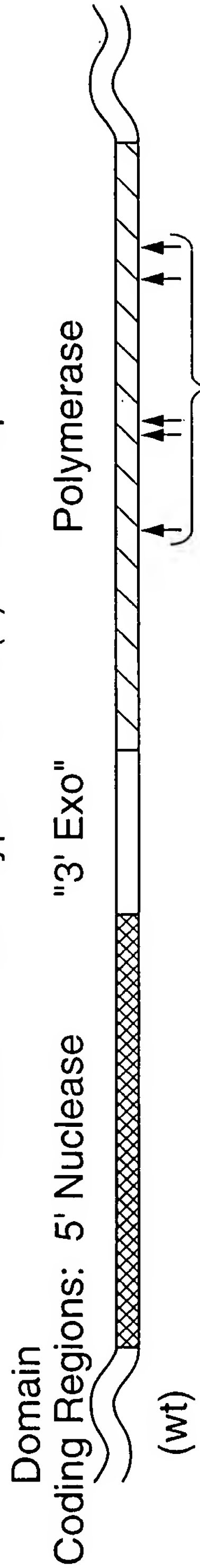


FIG. 3A

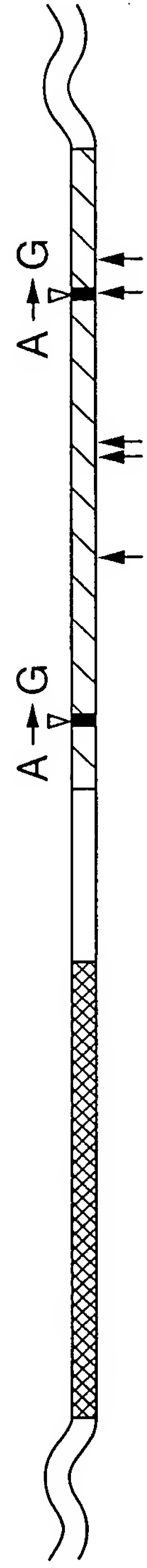


FIG. 3B

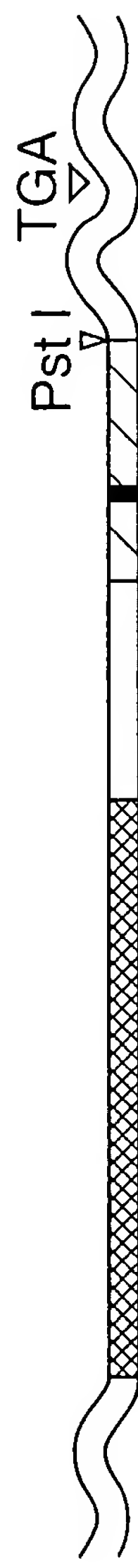


FIG. 3C

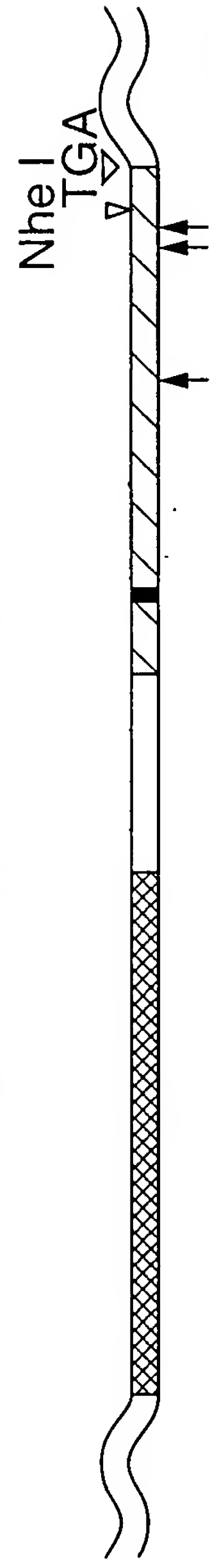


FIG. 3D

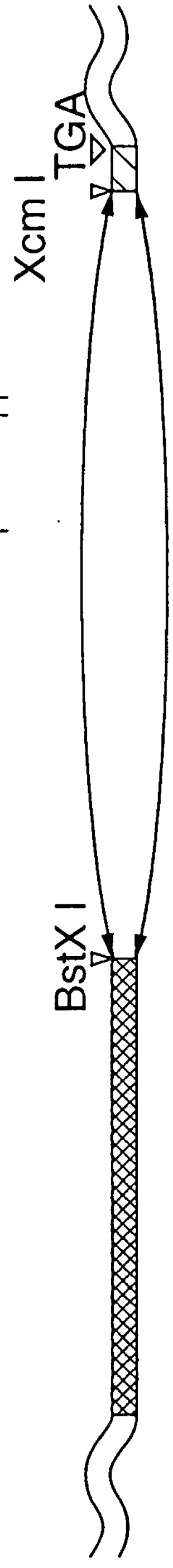


FIG. 3E

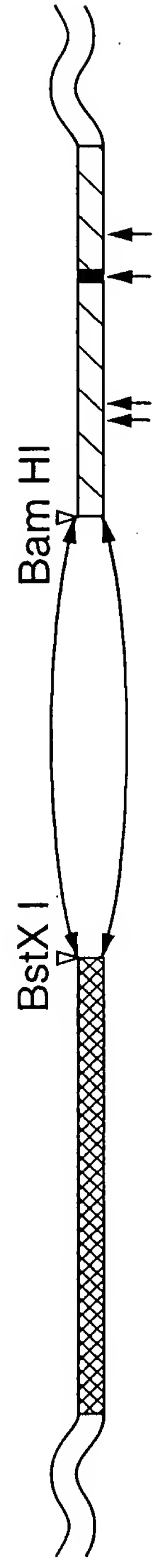


FIG. 3F

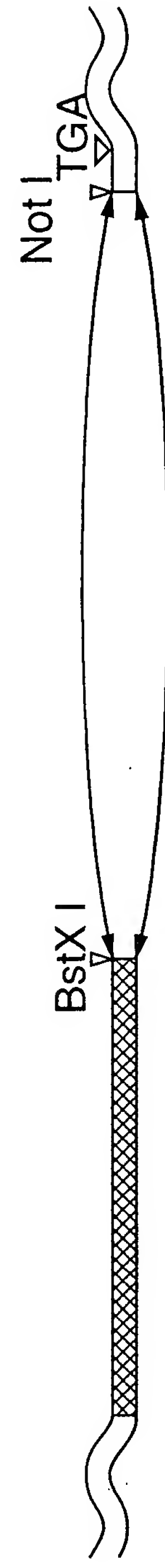
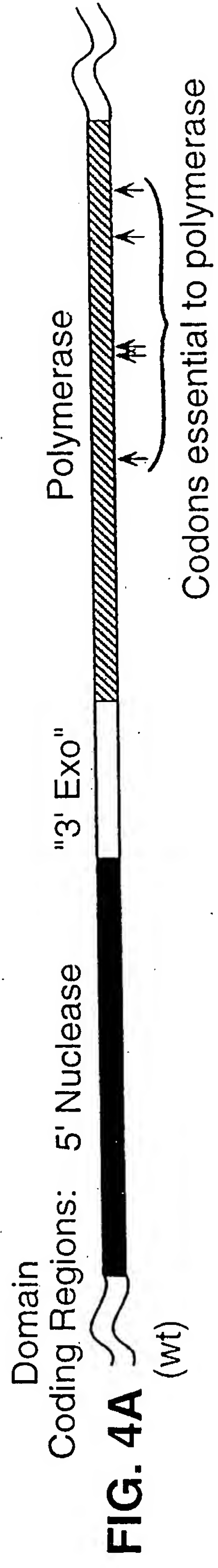


FIG. 3G

Genes for Wild-Type and Pol(-)DNAPTfl



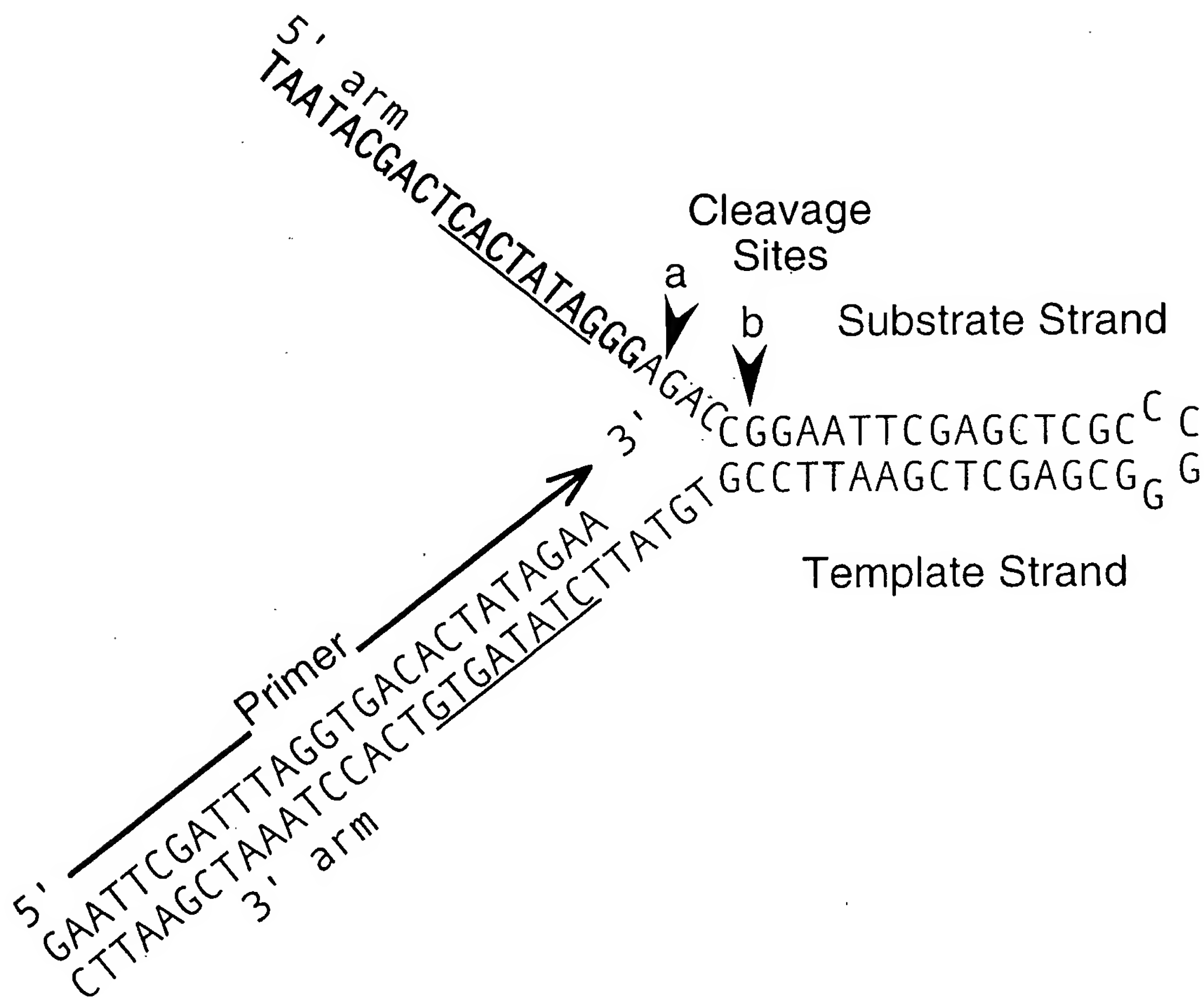
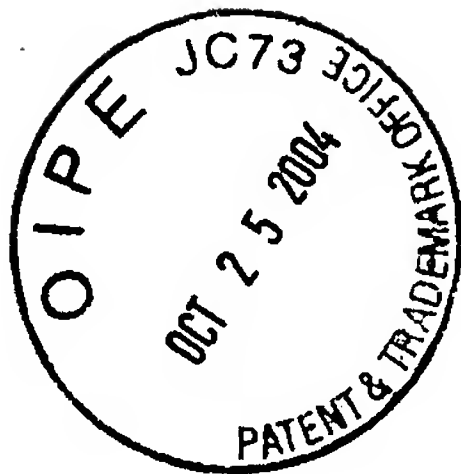


FIG. 5

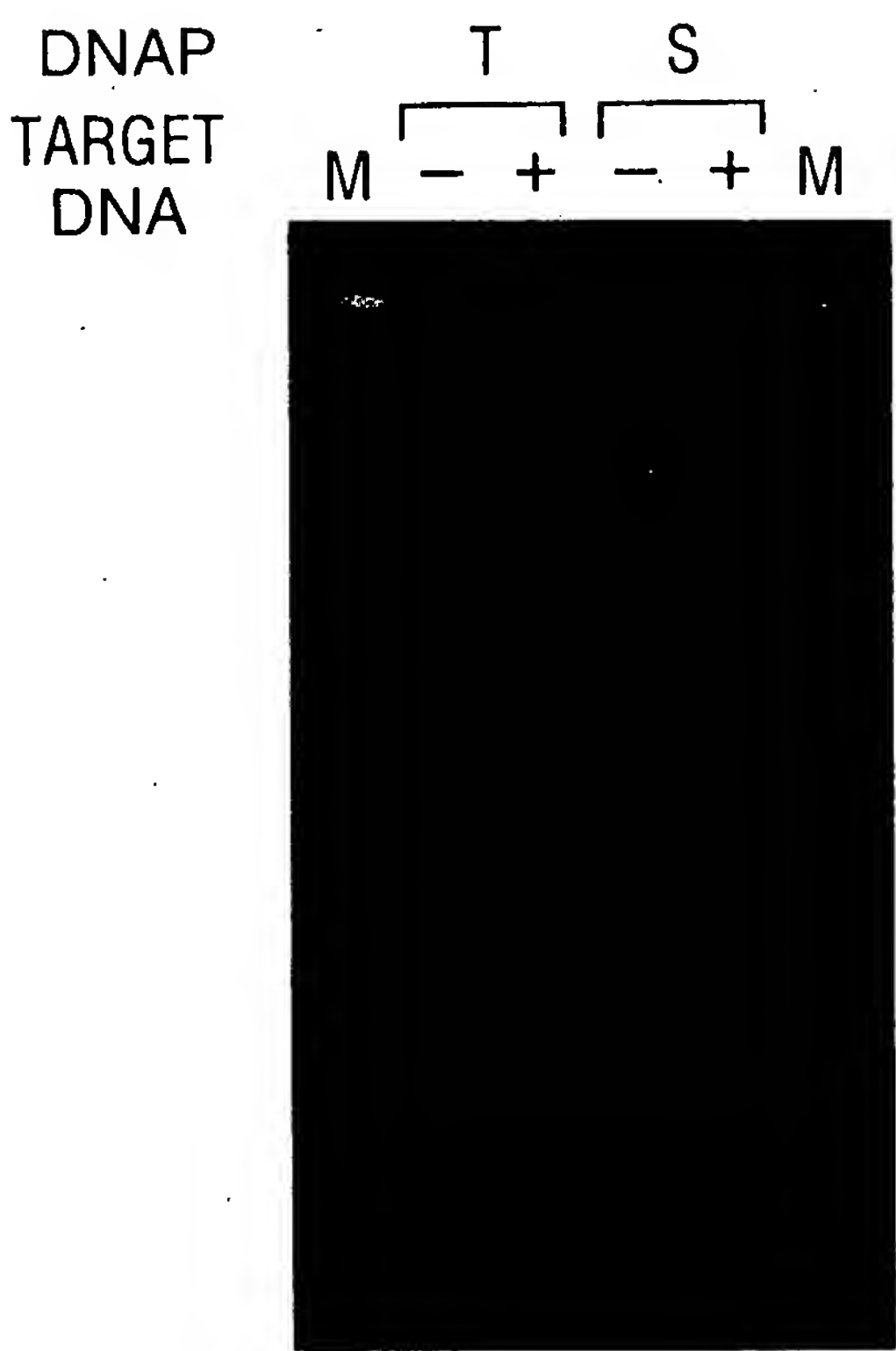
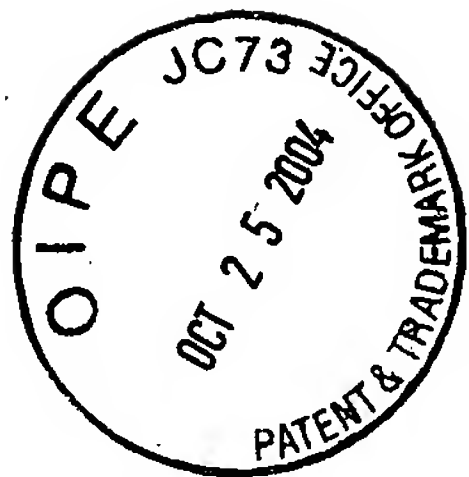


FIG. 6

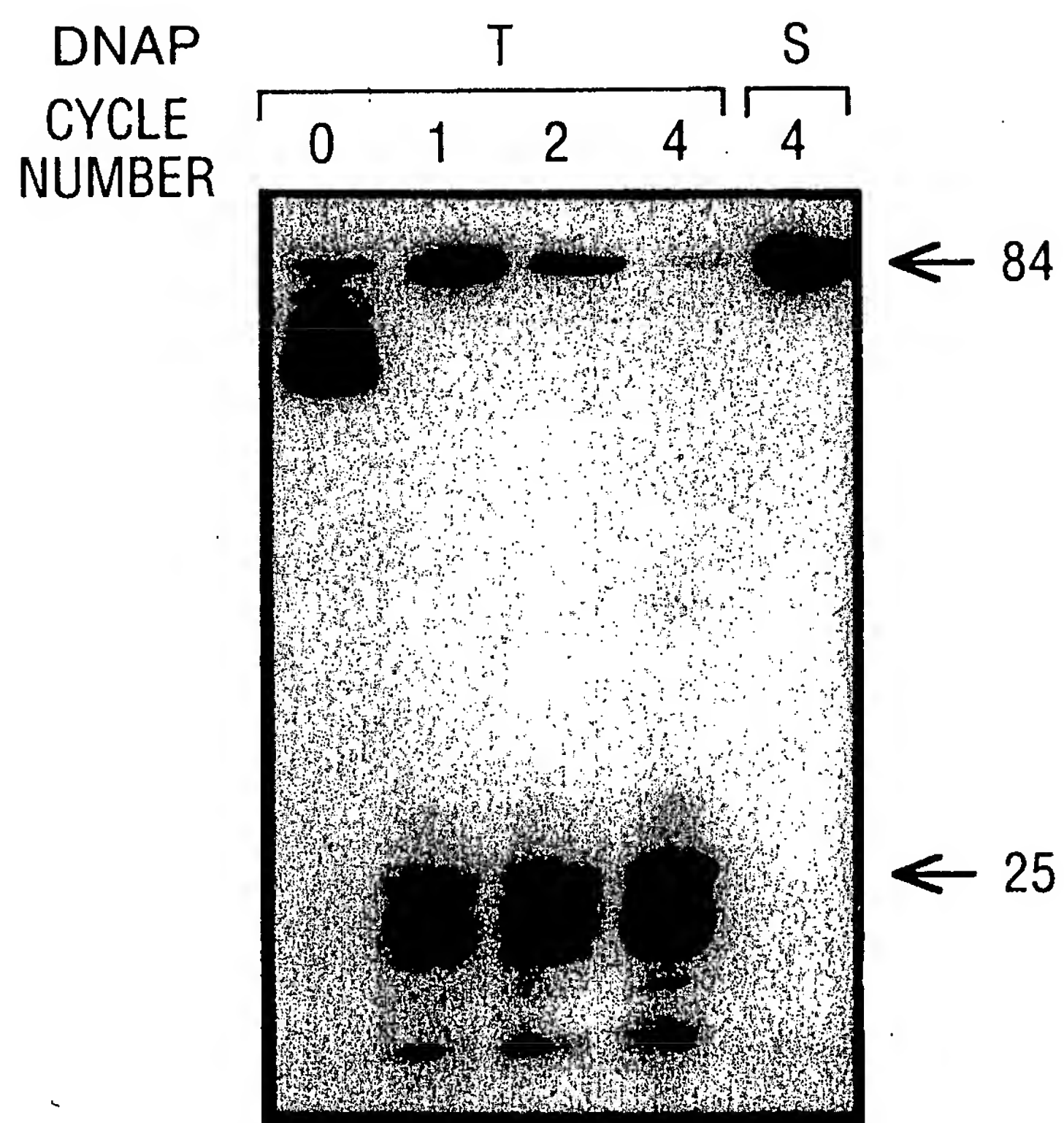
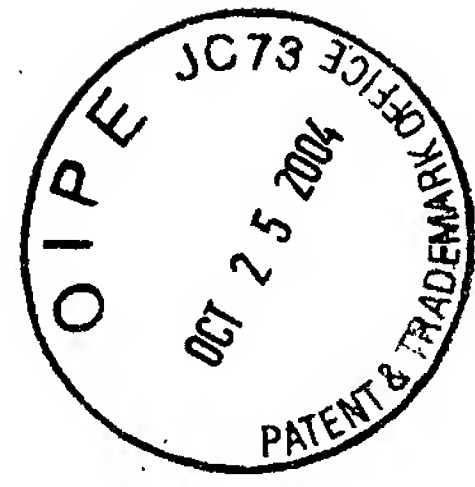


FIG. 7

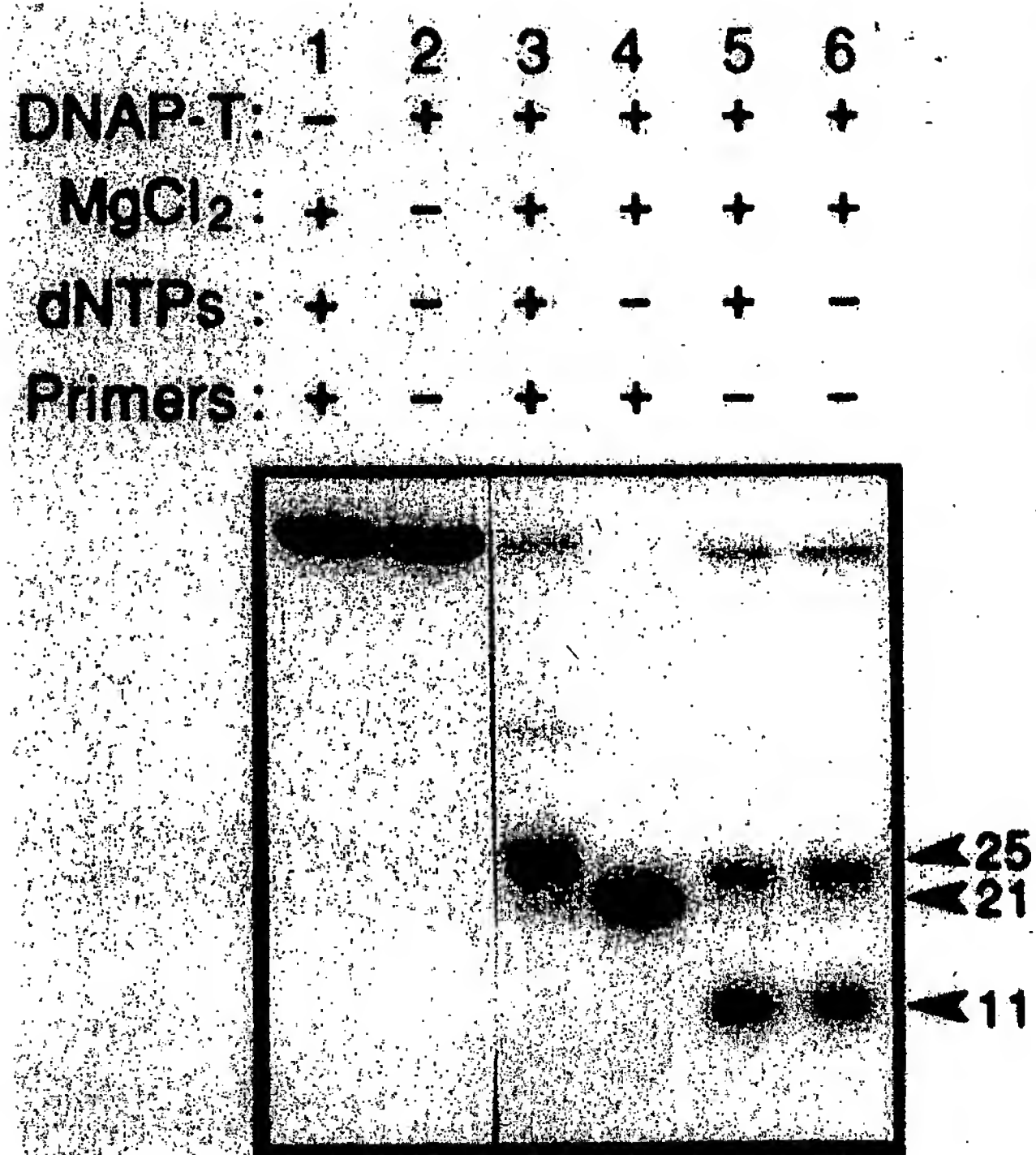


FIG. 8A

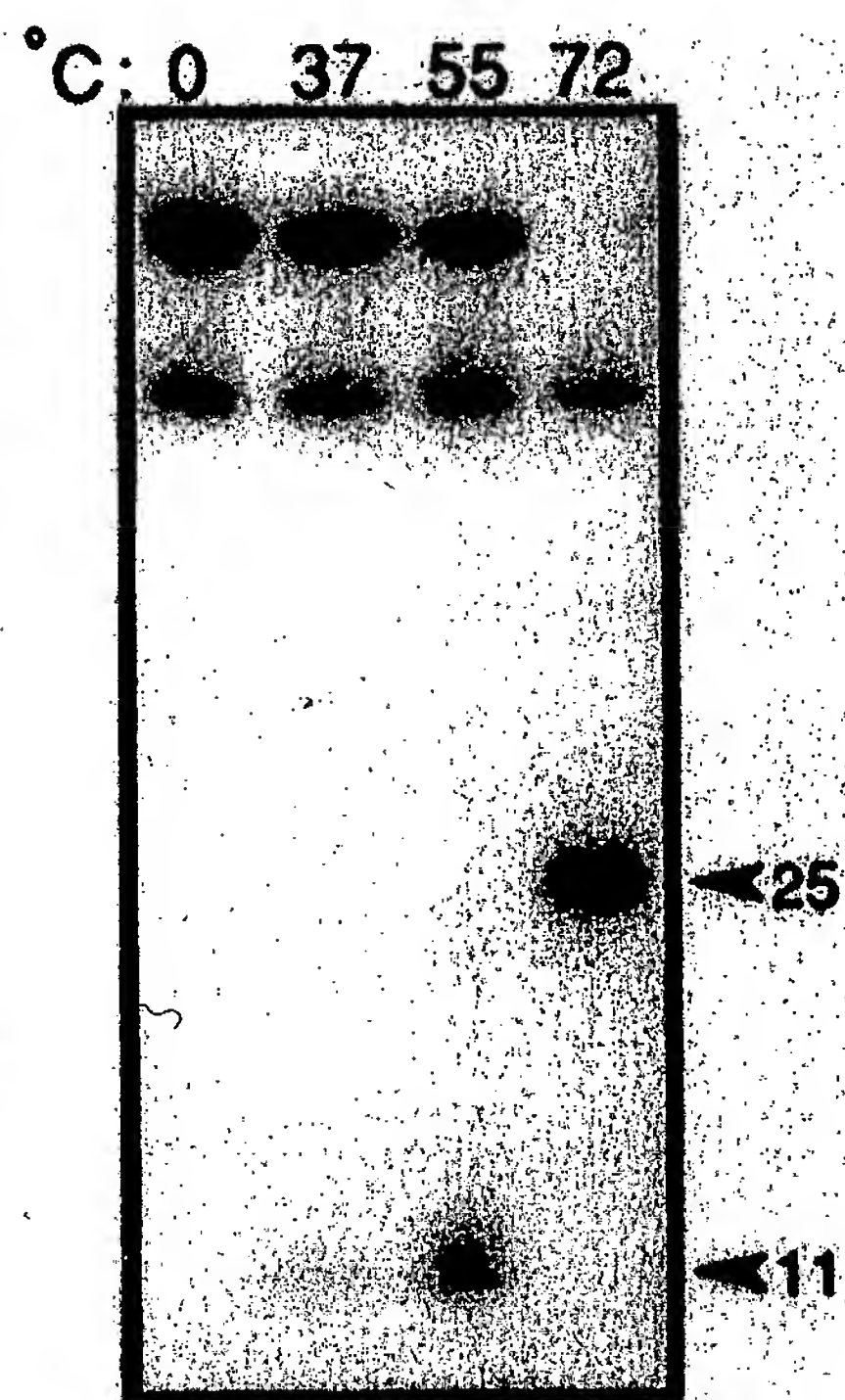
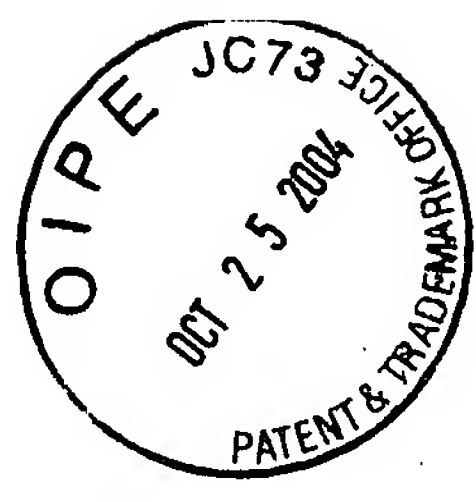


FIG. 8B



| + PRIMER | | | | | | | | | | -PRIMER | | | | | | | |
|--------------|---|---|-----|---|---|---|----|---|--|--------------|---|---|----|----|----|----|---|
| └──────────┘ | | | | | | | | | | └──────────┘ | | | | | | | |
| t (MIN): | M | 0 | 0.5 | 1 | 3 | 5 | 10 | M | | M | 0 | 5 | 10 | 20 | 40 | 60 | M |

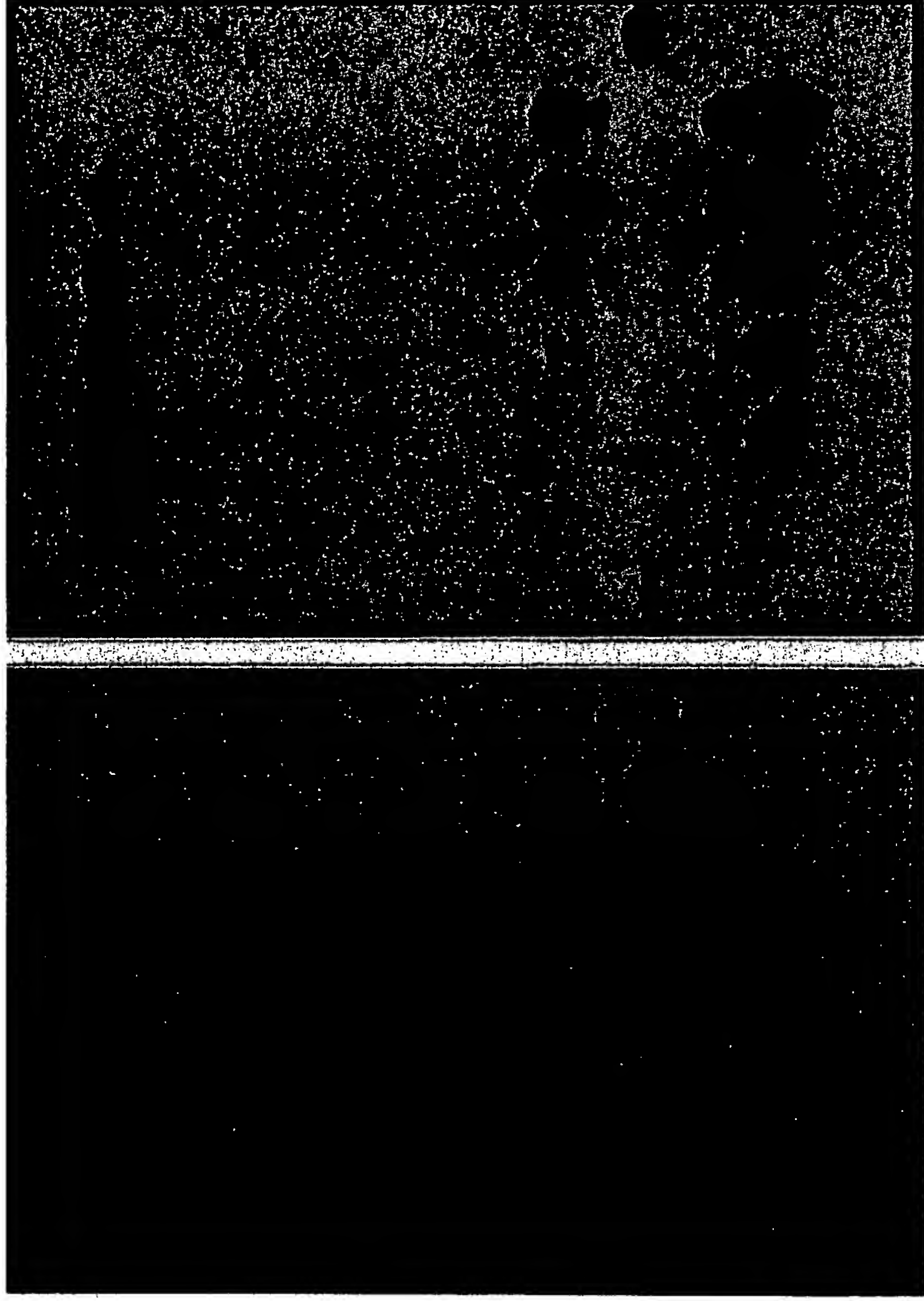


FIG. 9A

FIG. 9B

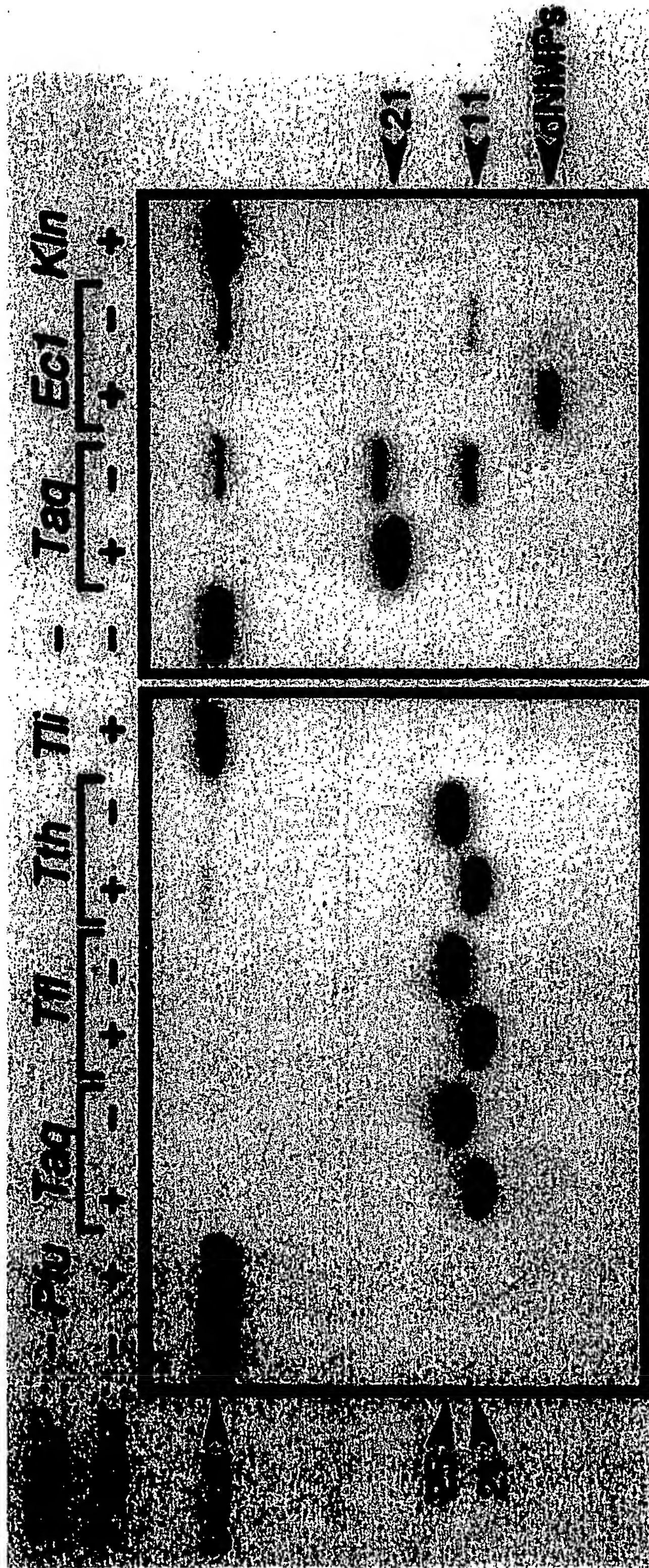


FIG. 10B

FIG. 10A

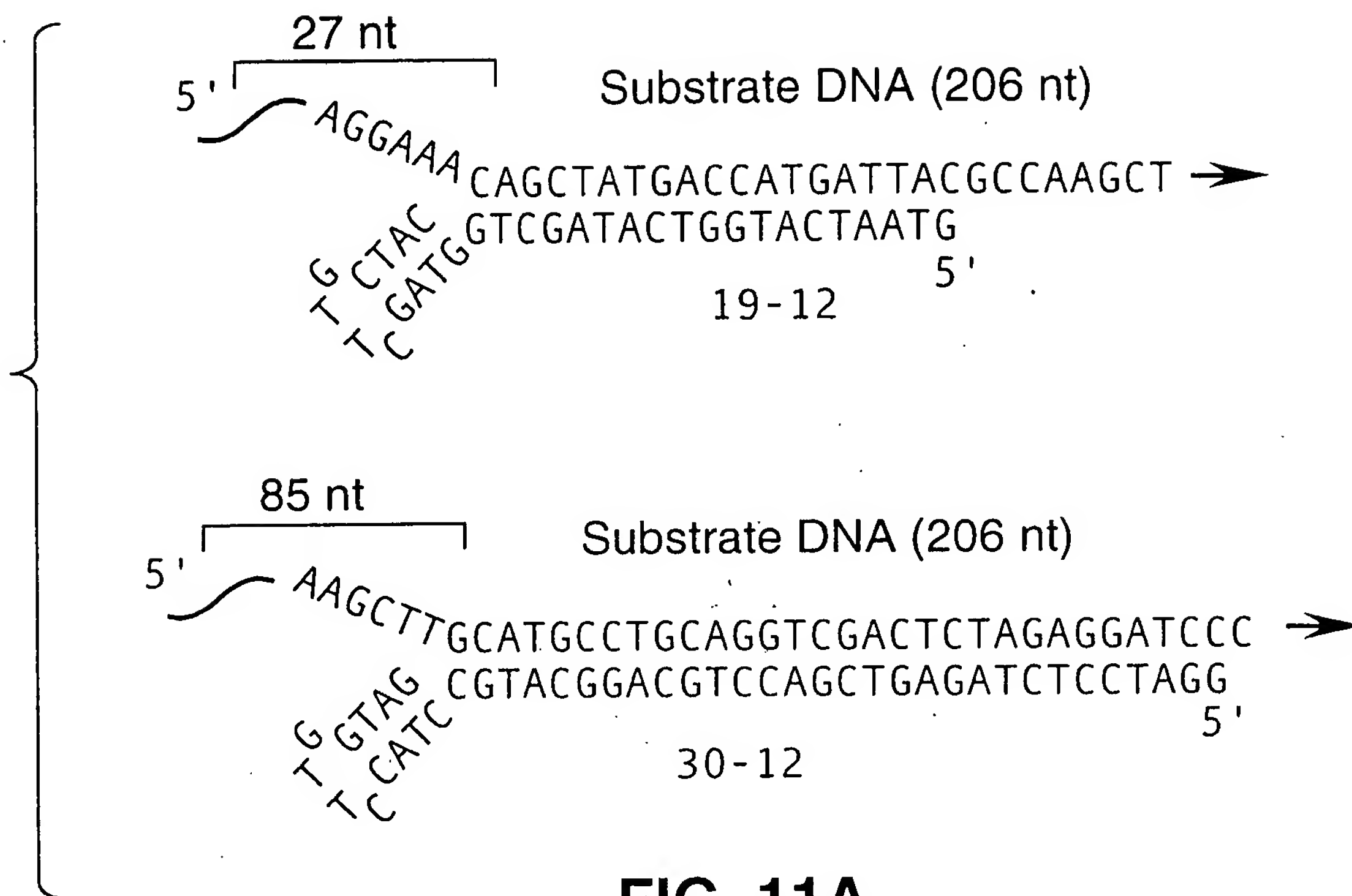
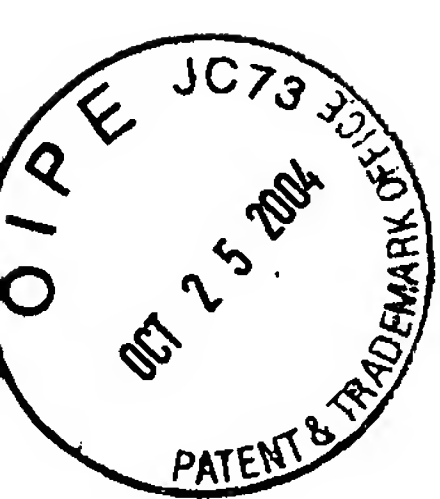


FIG. 11A

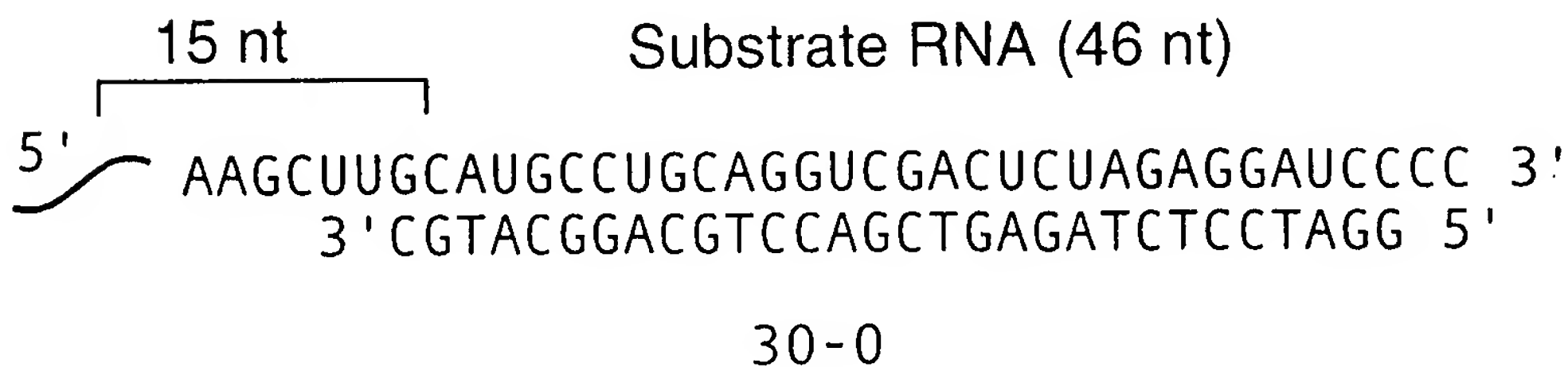


FIG. 12A

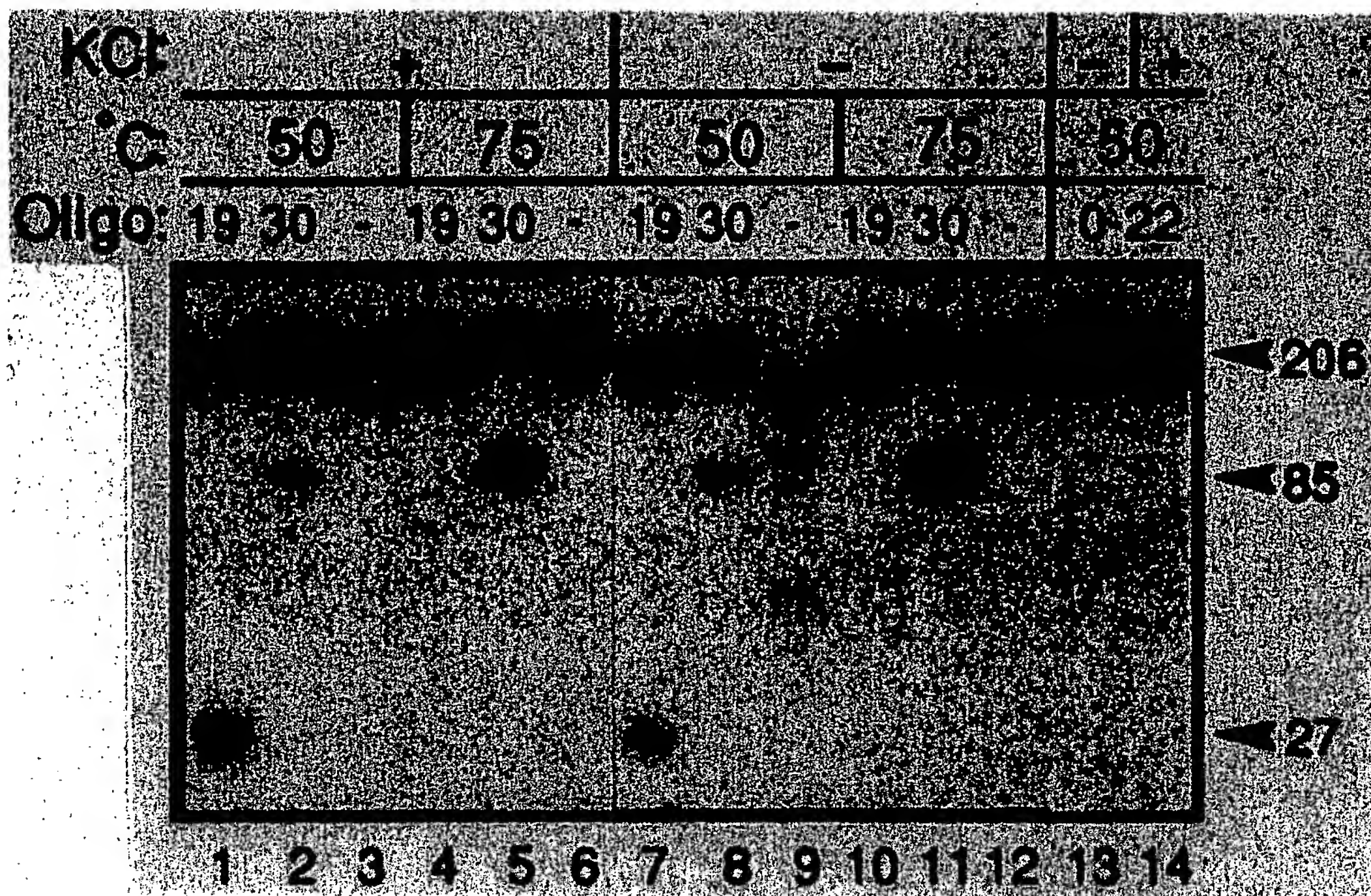


FIG. 11B

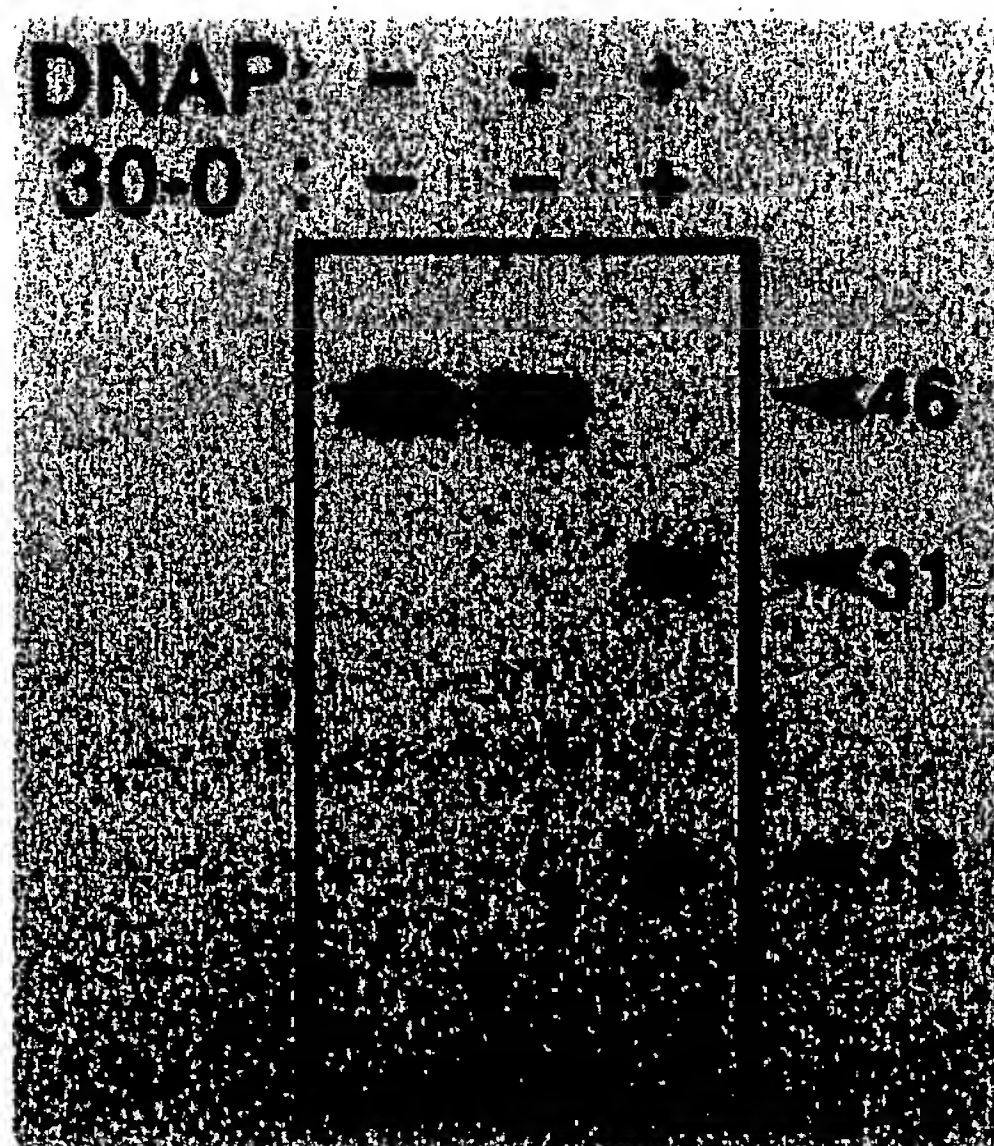


FIG. 12B

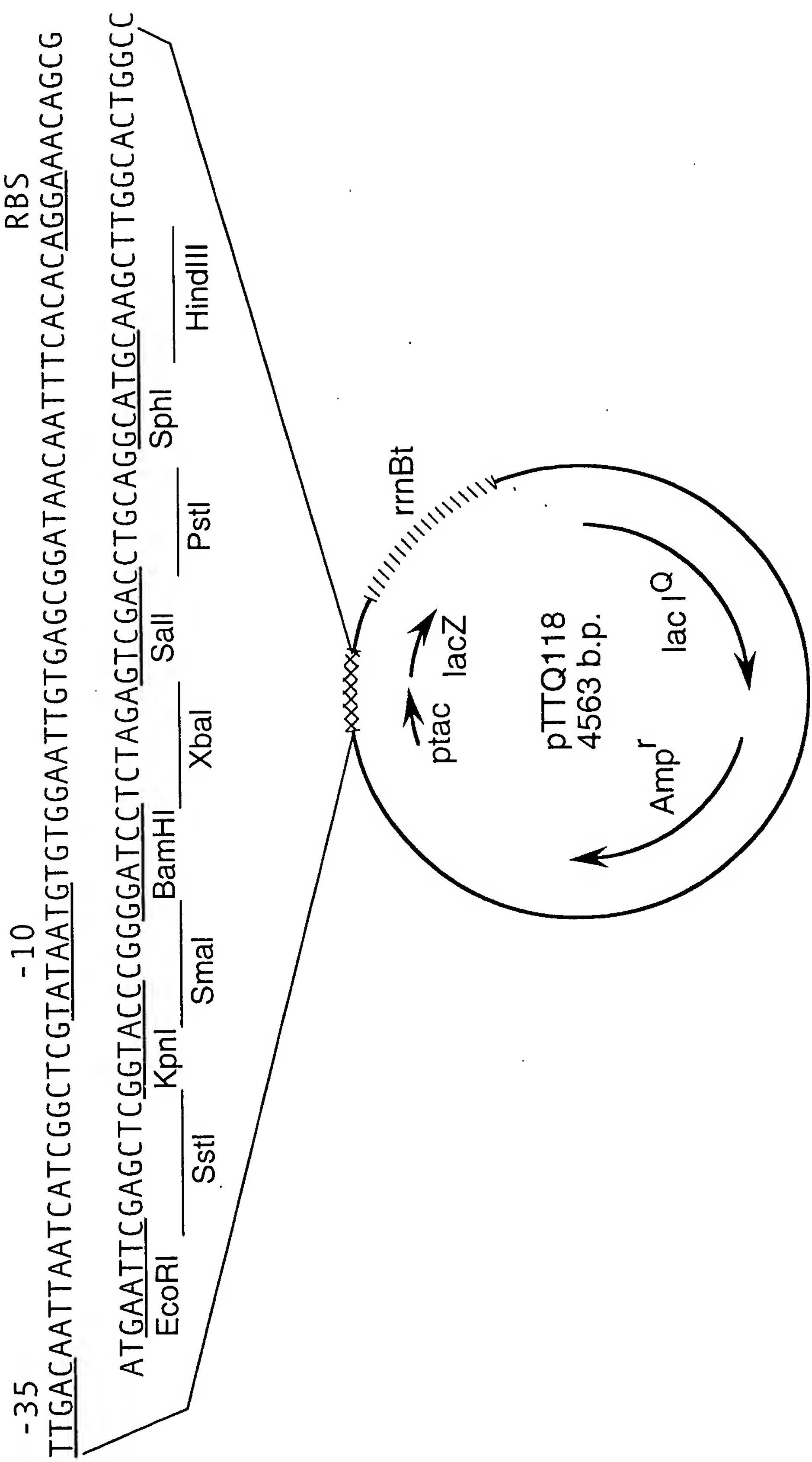


FIG. 13

By: _____

T7 Promoter

Xbal

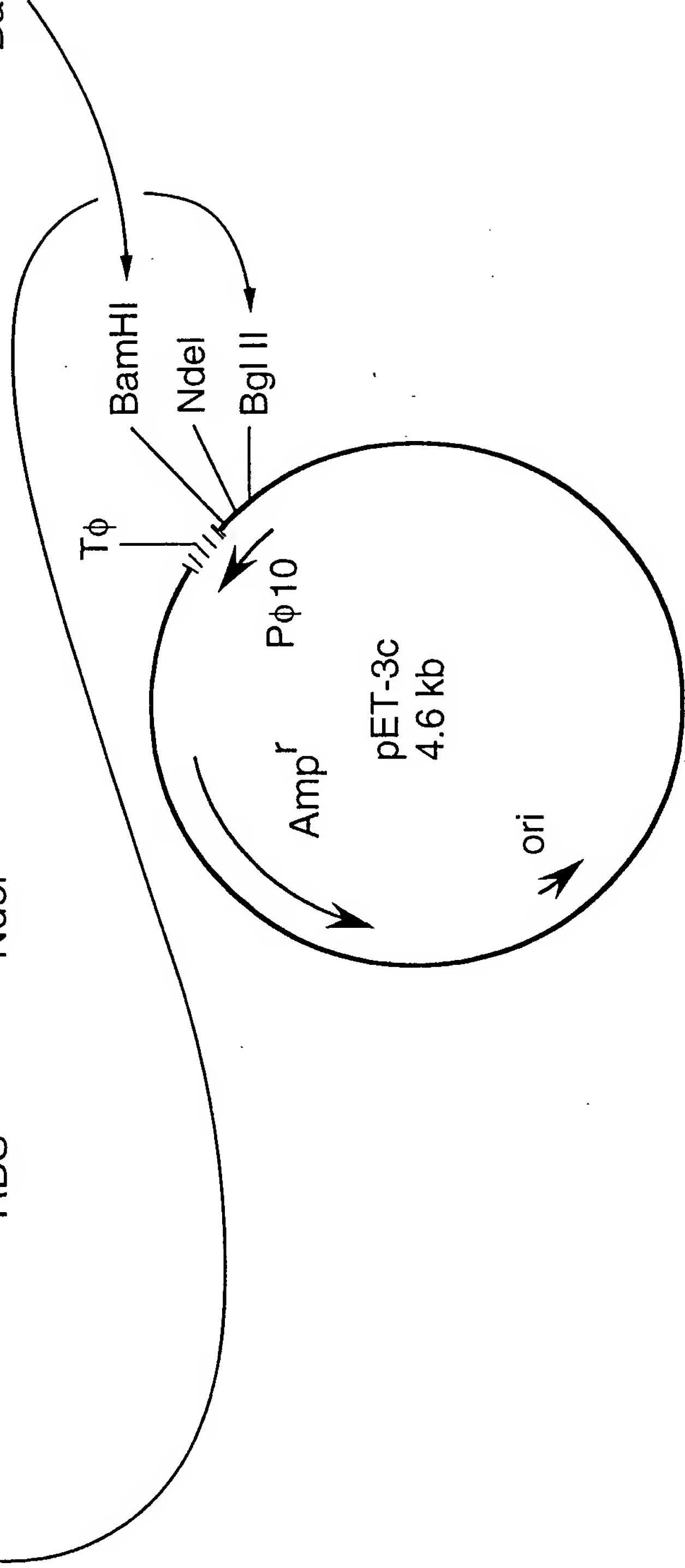
MetAlaSer...

AACTTTAAGAAGGAGATATACATATGGCTAGCATGACTGGTGGACAGCAAATGGGTCCGGCT

RBS

Ndel

BamHI

Amp^r

P010

pET-3c
4.6 kb

TI

BamHI

Idel

Bali

P_{φ10} : Bacteriophage T7 φ10 promoter RBS: Ribosome binding site

To: T7 ϕ Terminator

RBS: Ribosome binding site

FIG. 14

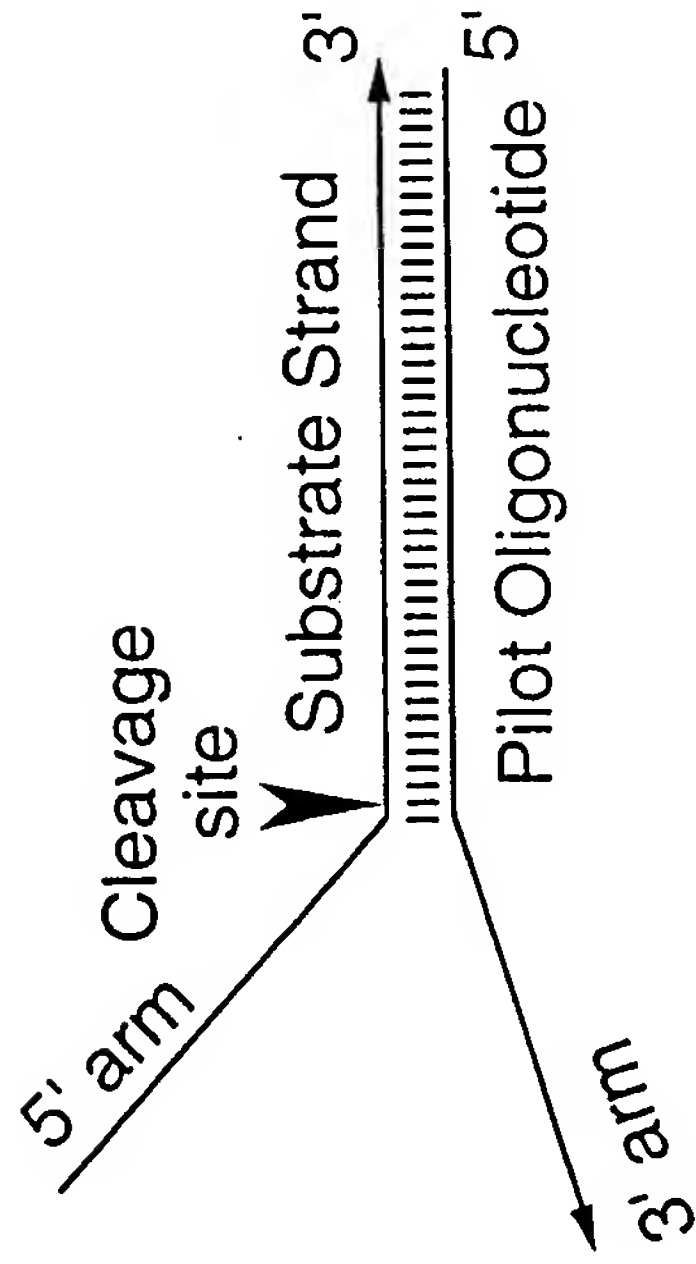


FIG. 15A

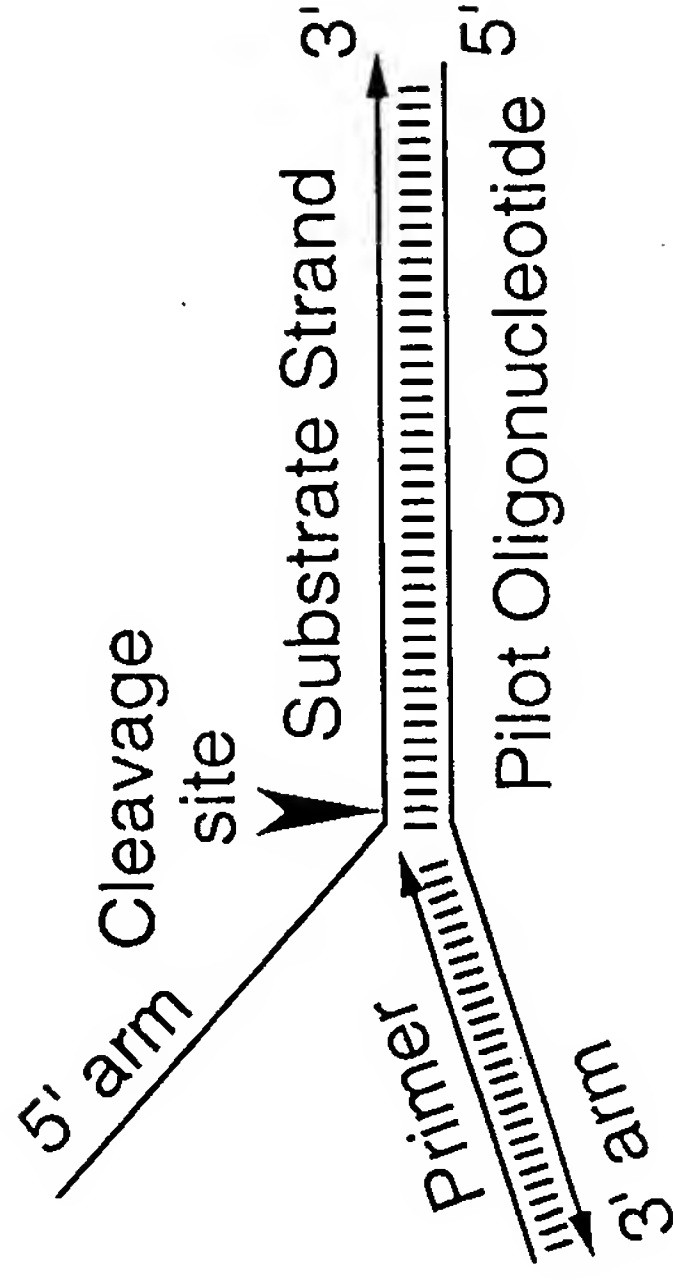


FIG. 15B

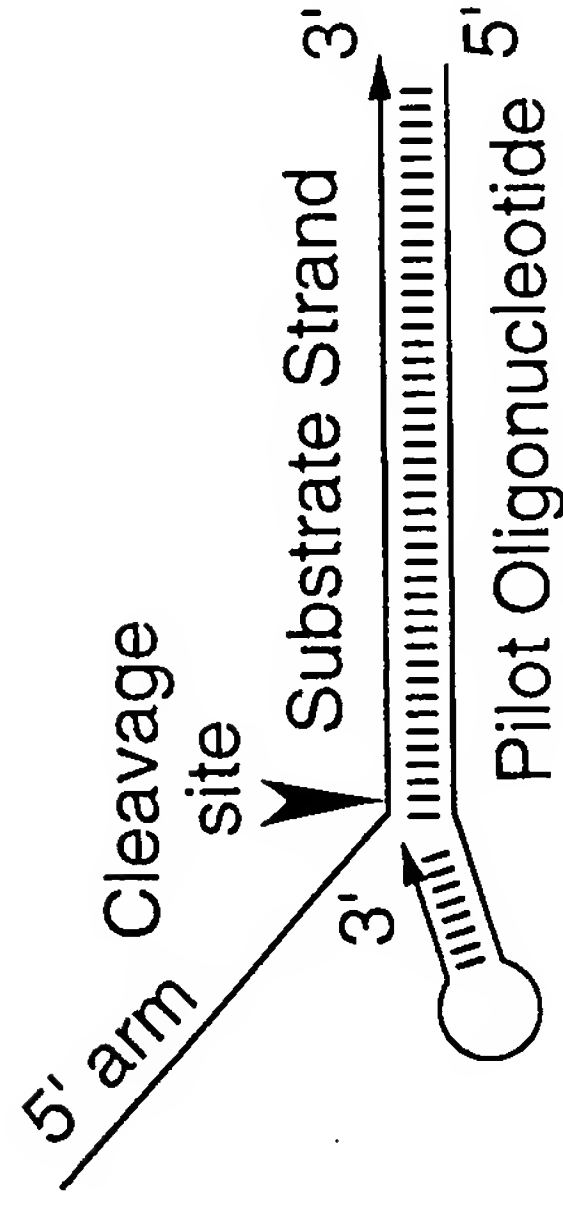


FIG. 15C

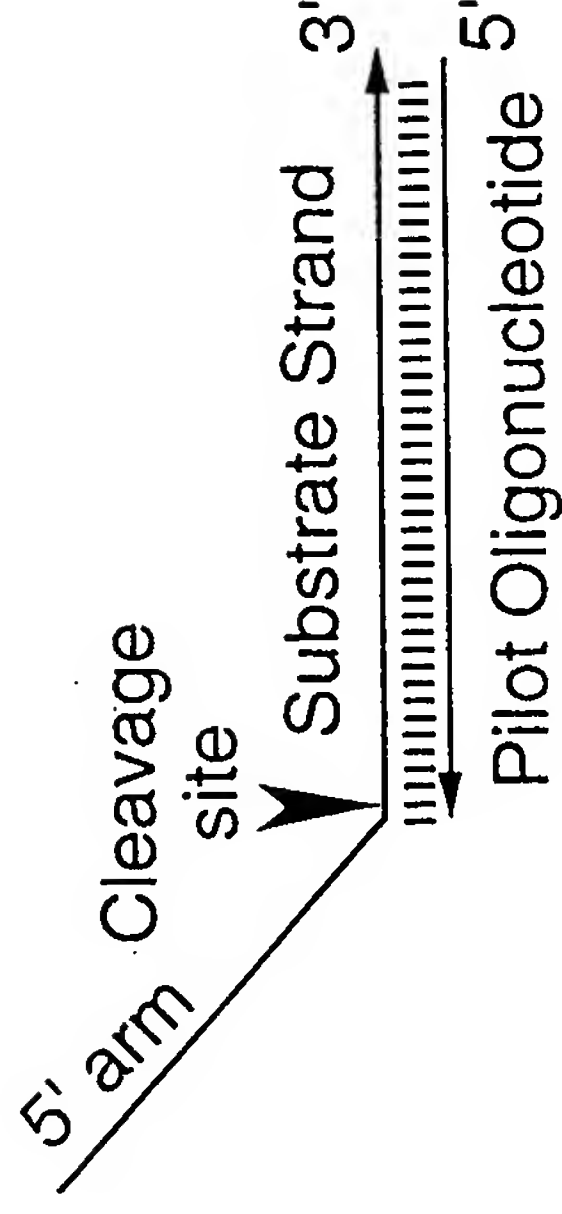


FIG. 15D

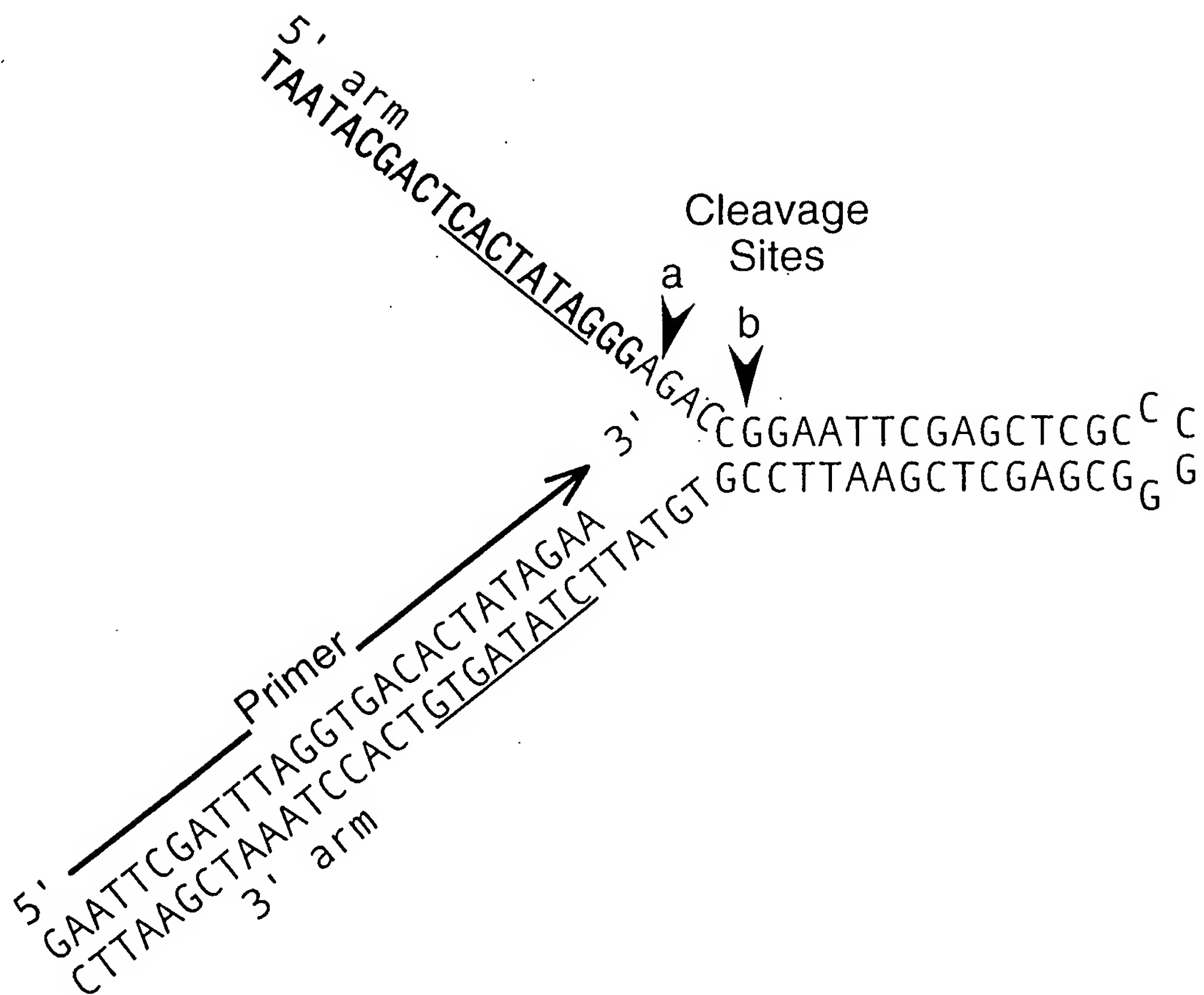
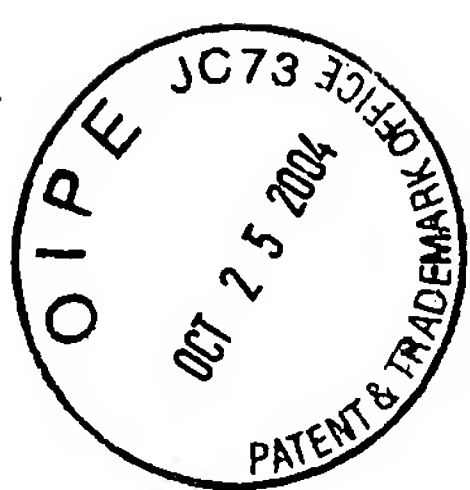


FIG. 15E

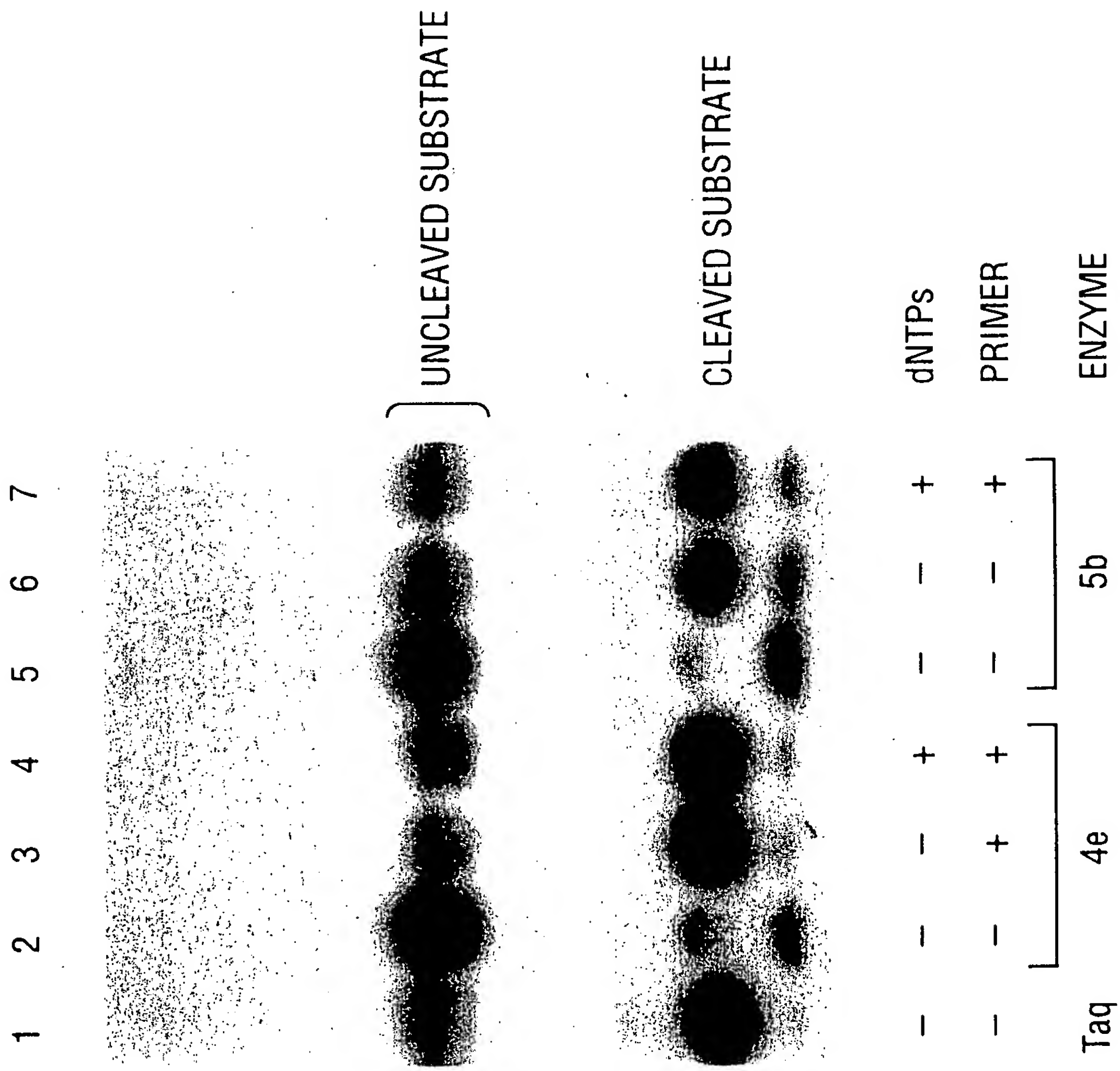


FIG. 16

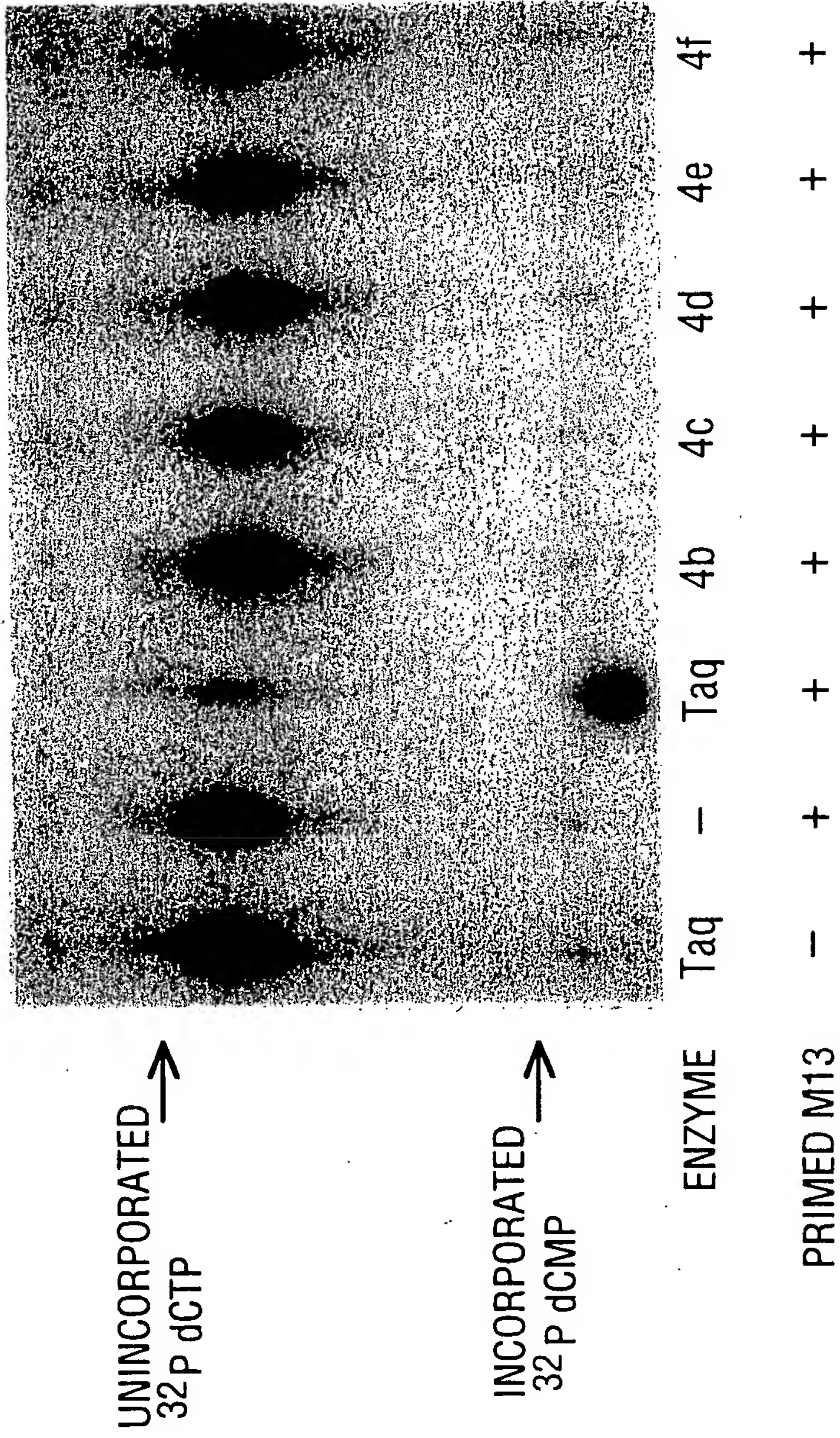


FIG. 17

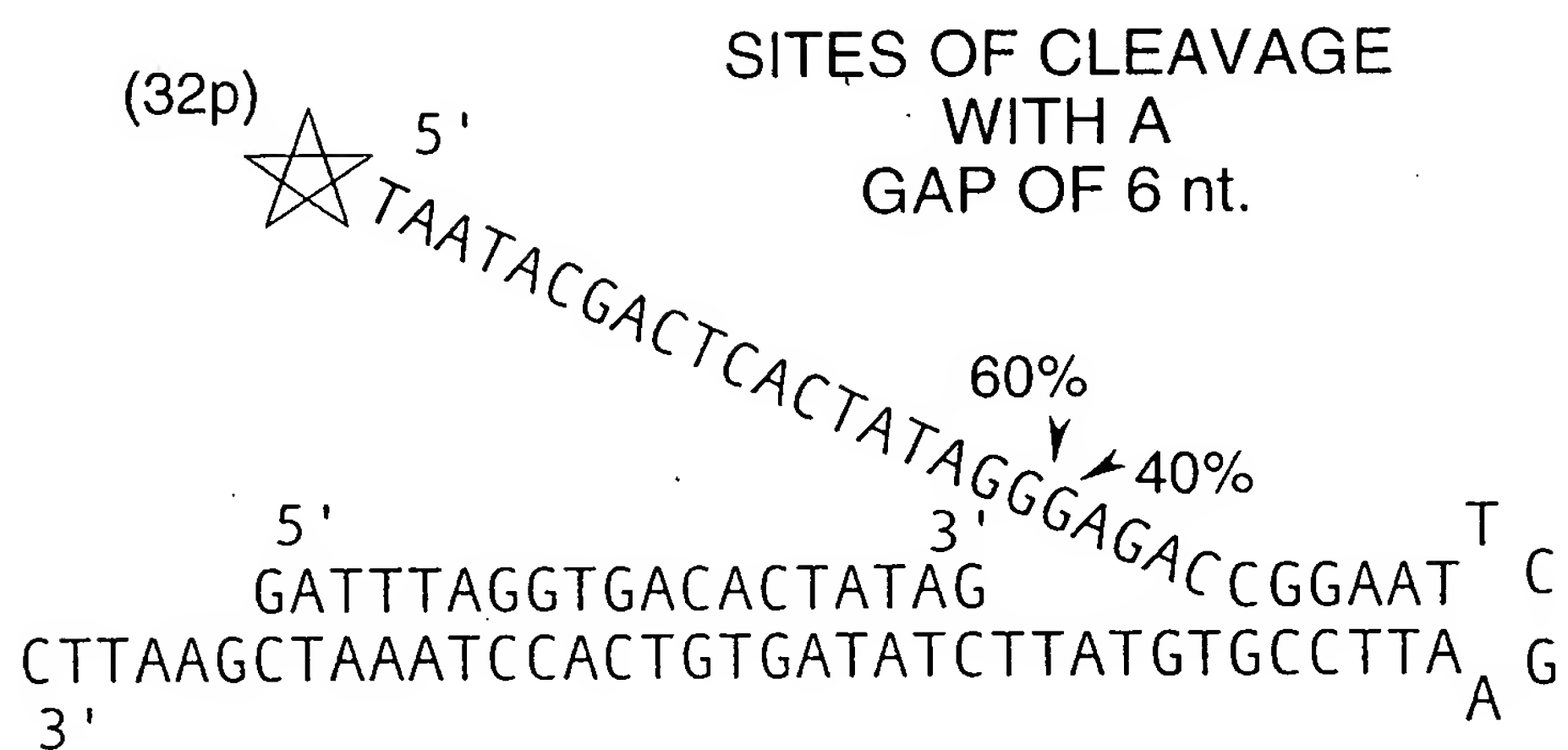
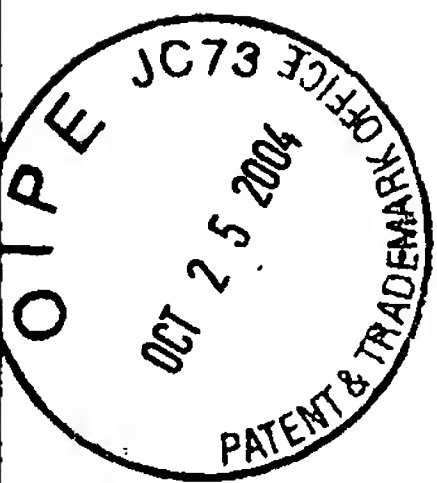


FIG. 18A

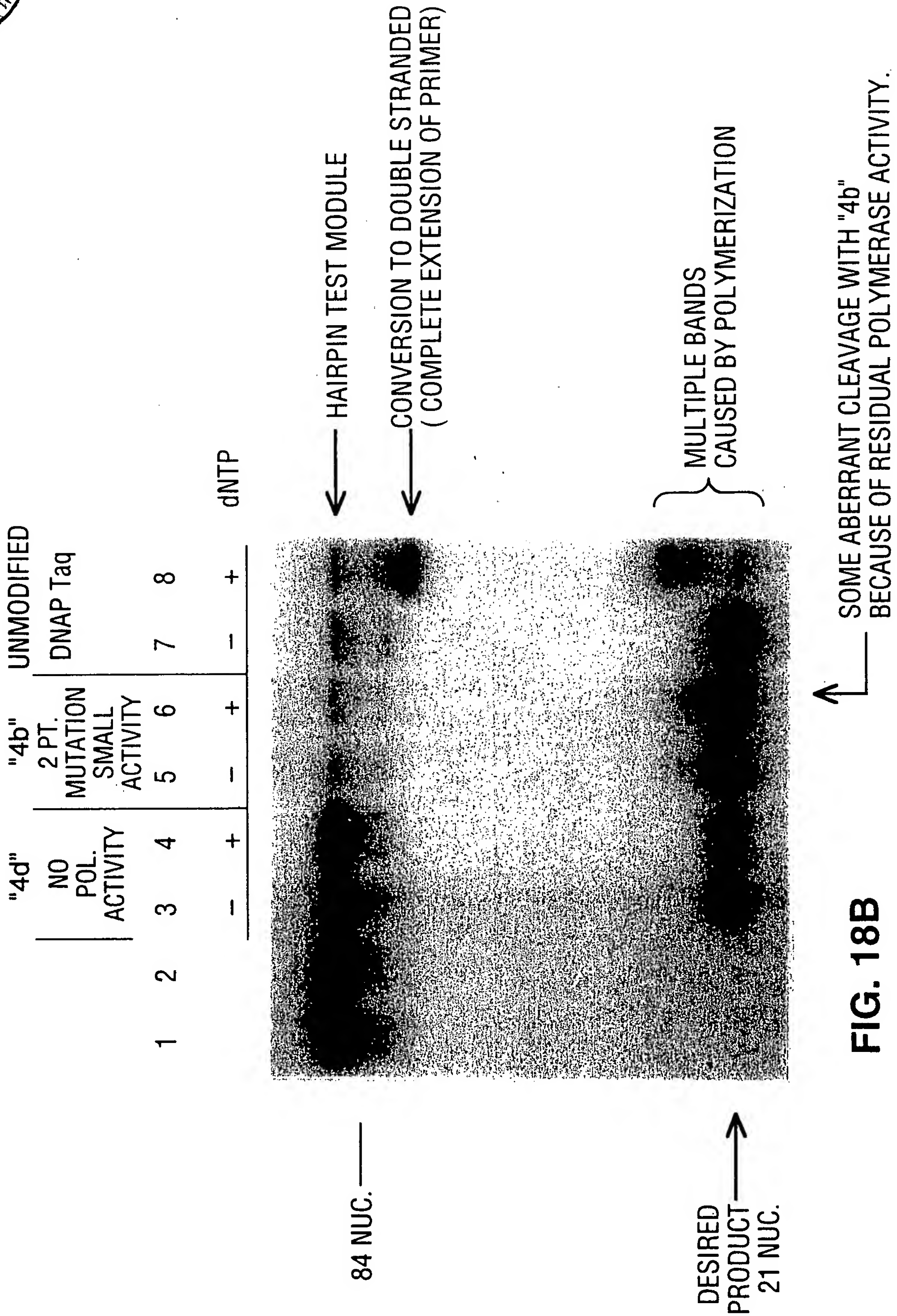


FIG. 18B

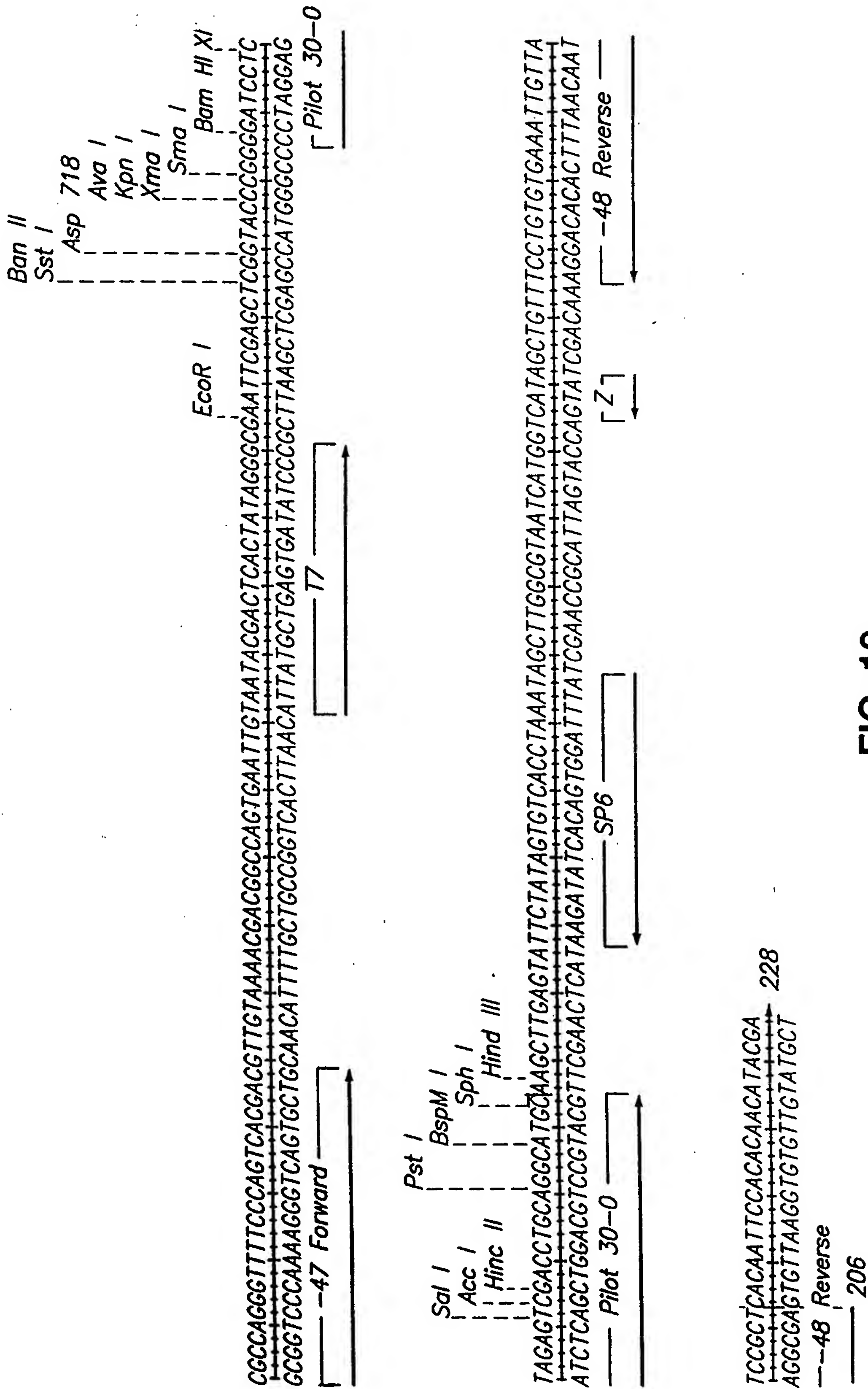
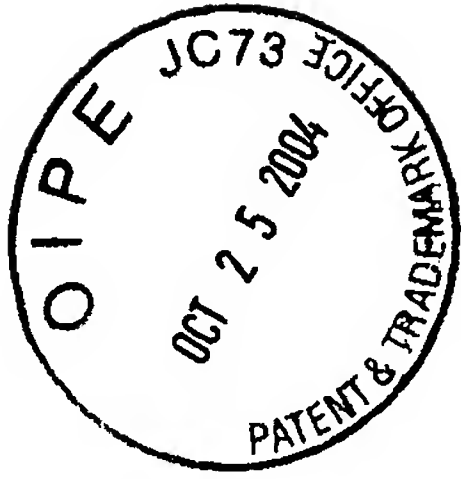


FIG. 19

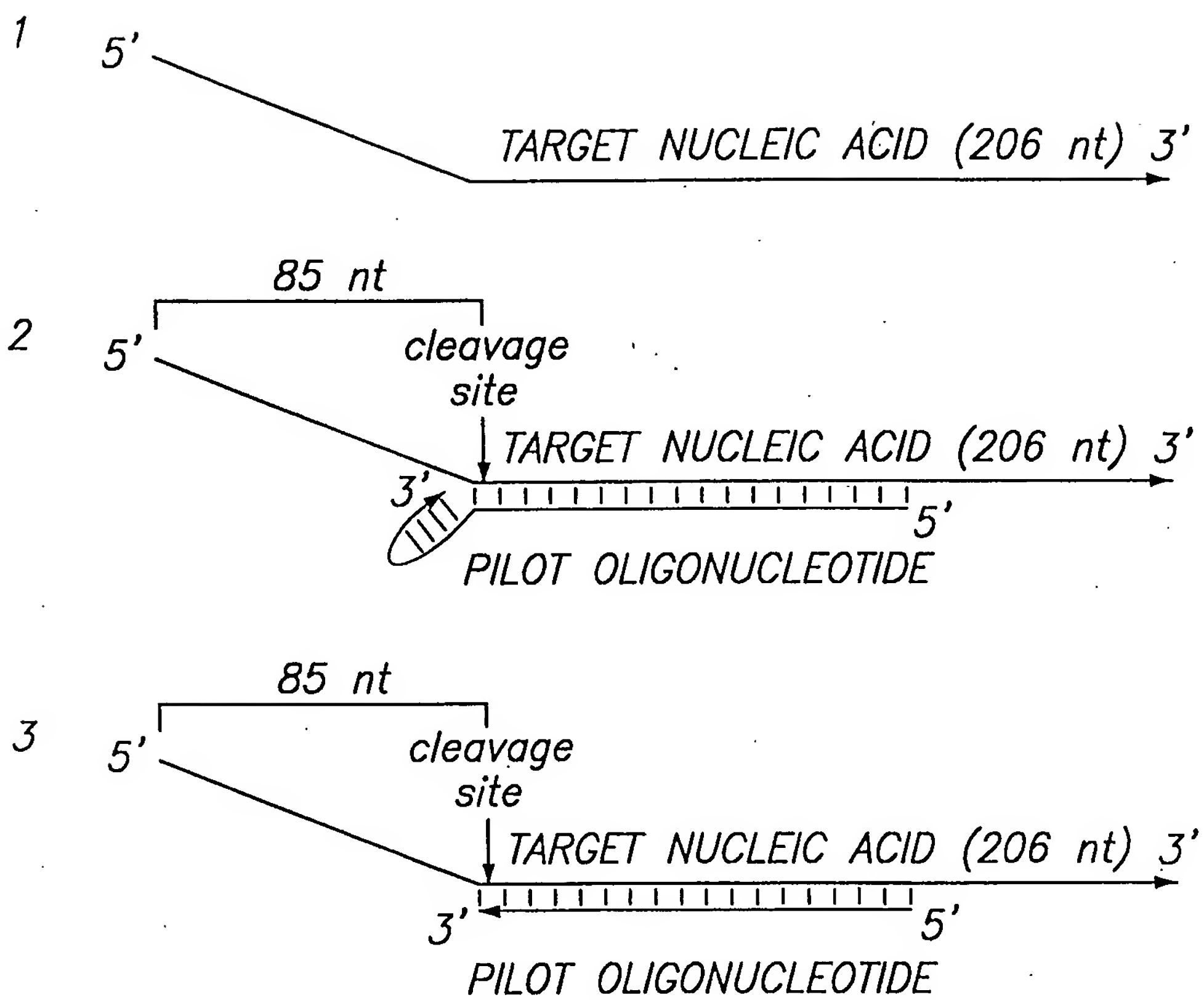
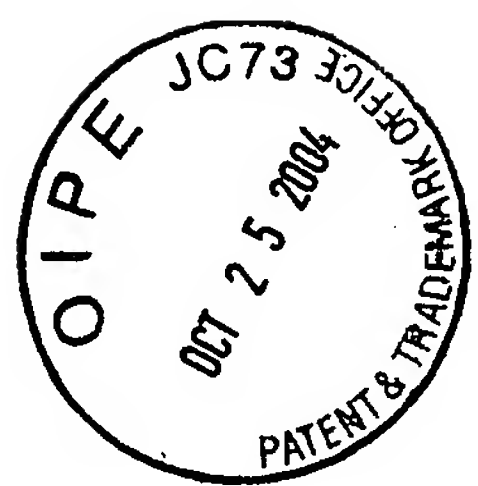


FIG. 20A

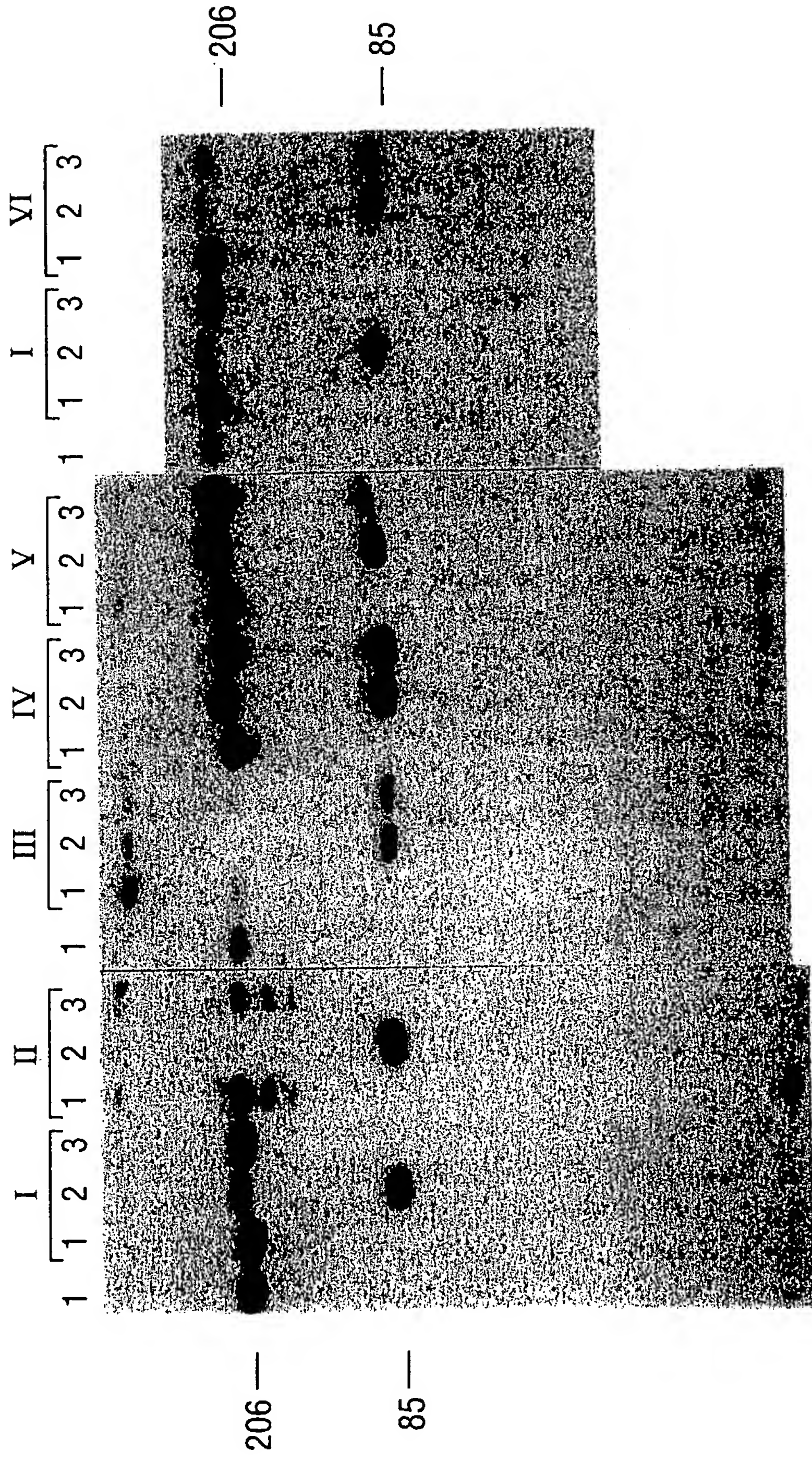
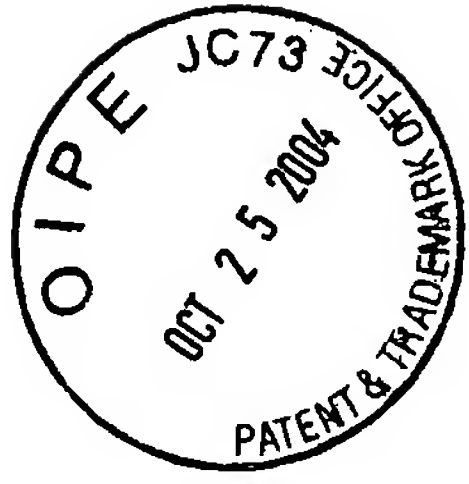


FIG. 20B

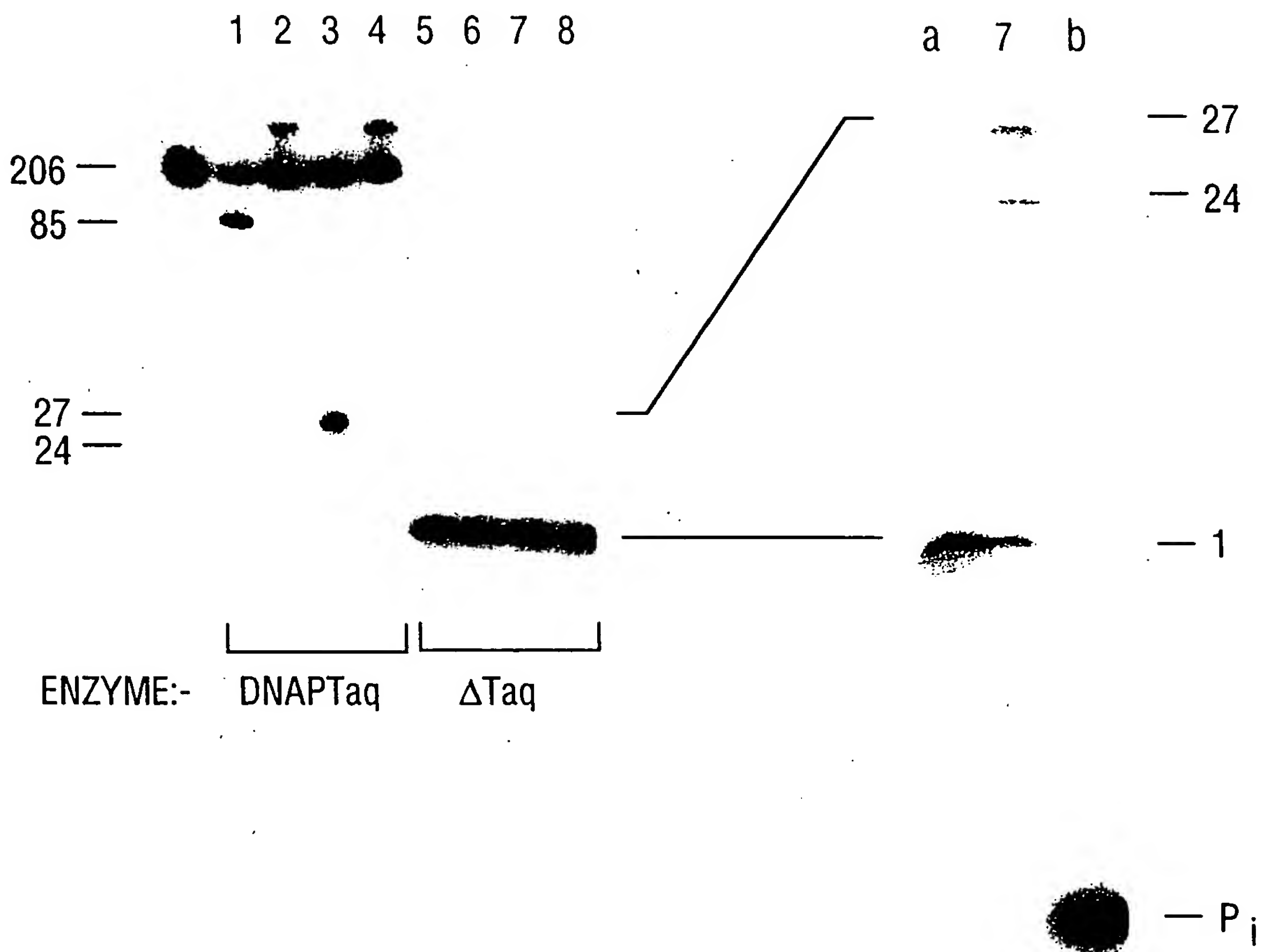
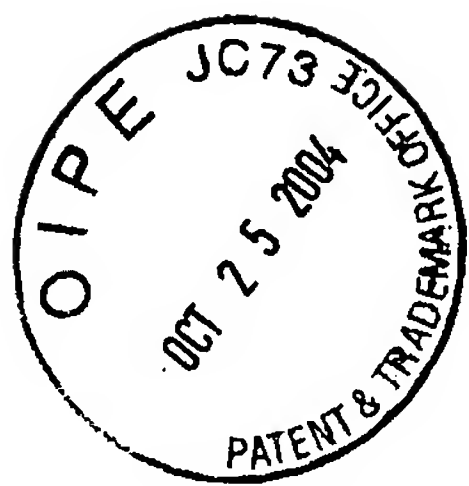


FIG. 21A

FIG. 21B

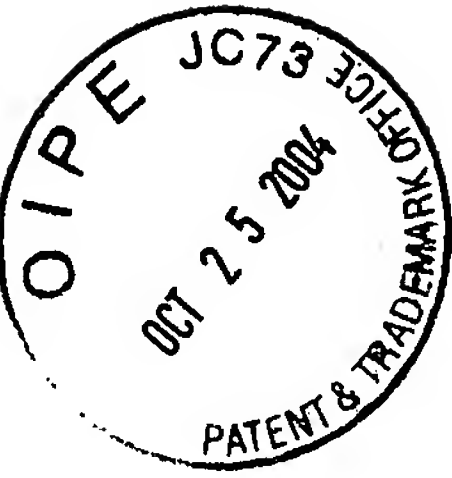


FIG. 22A

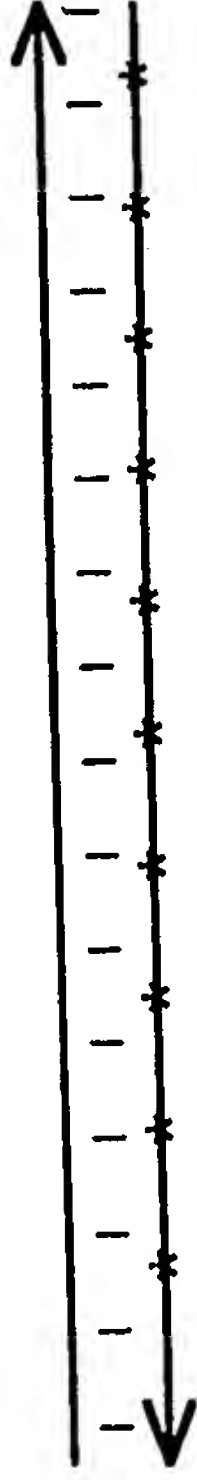


FIG. 22B

* = 32p



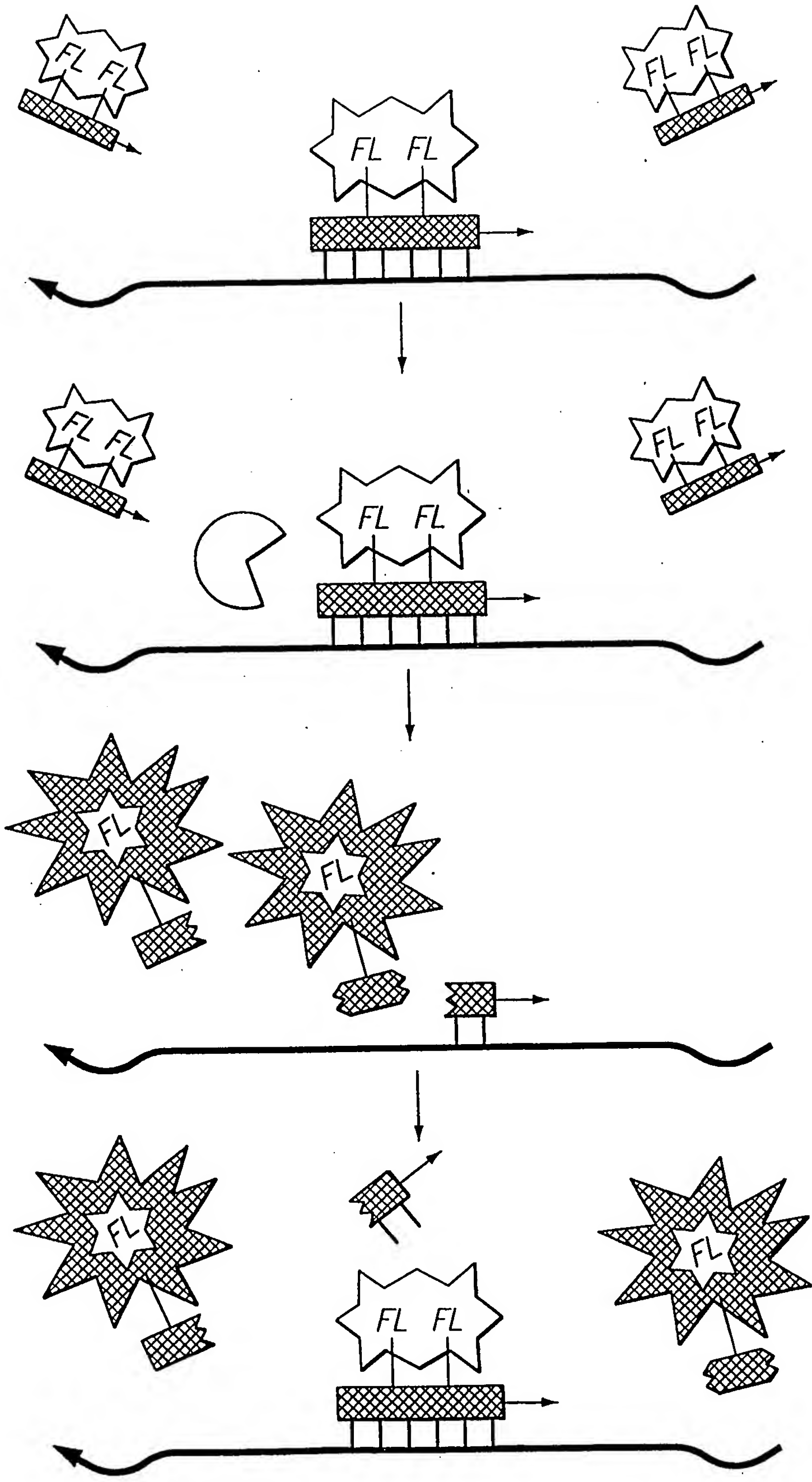


FIG. 23

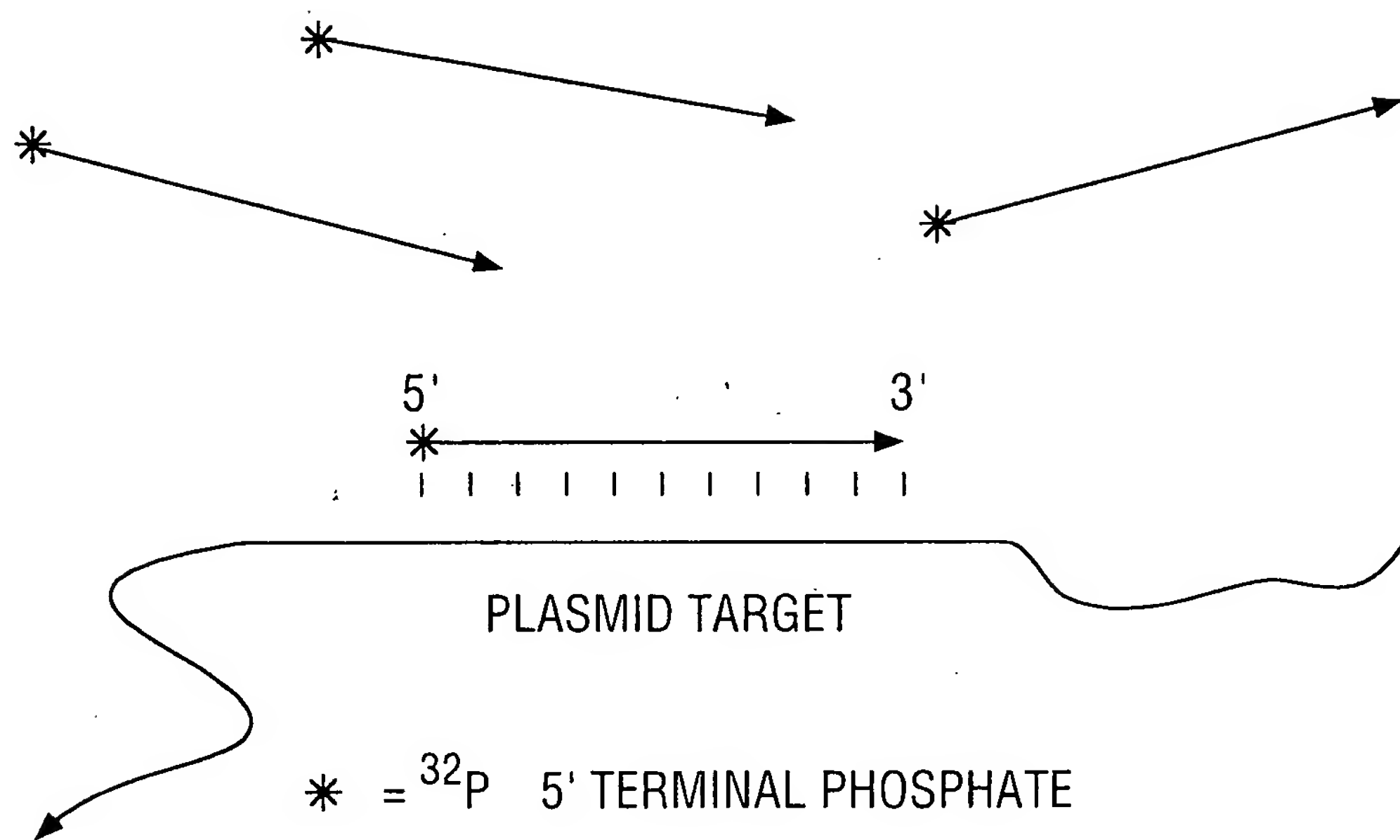
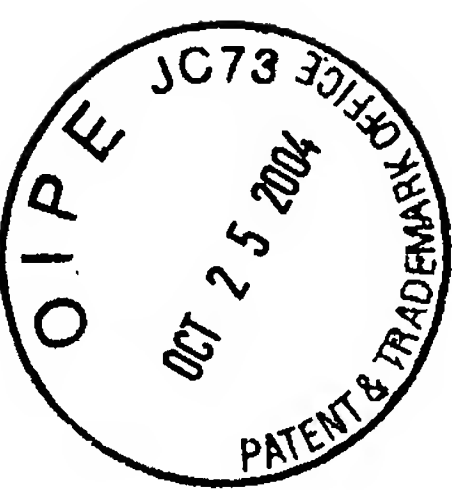
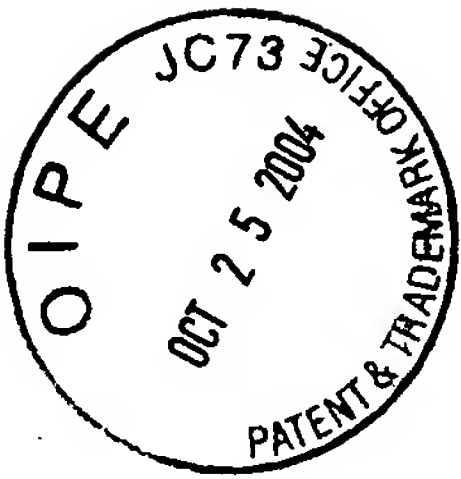


FIG. 24A



M 1 2 3 4 5 6



— 21

— 1

FIG. 24B

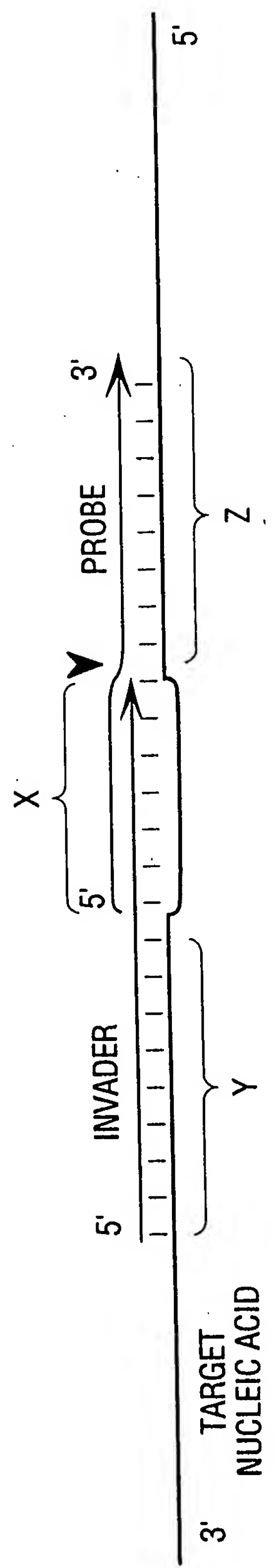
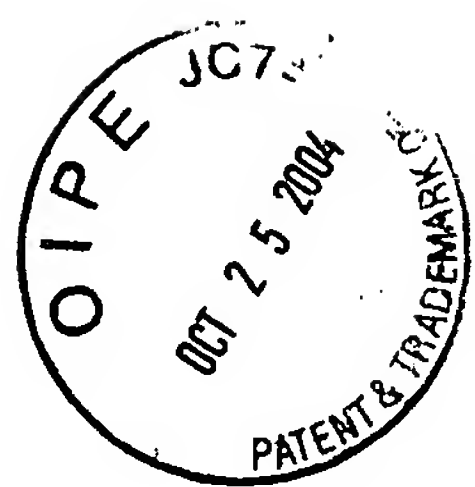


FIG. 25

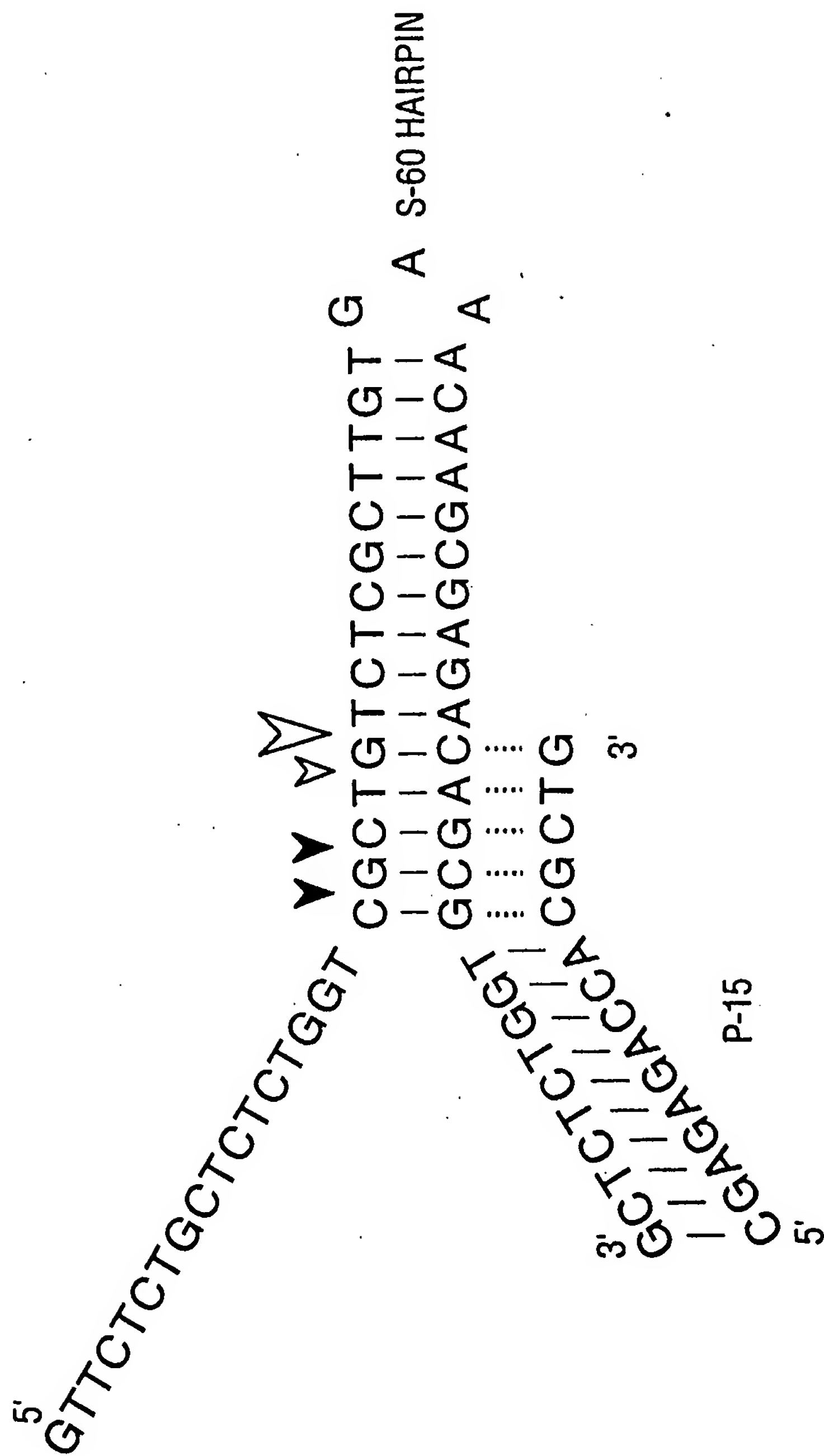
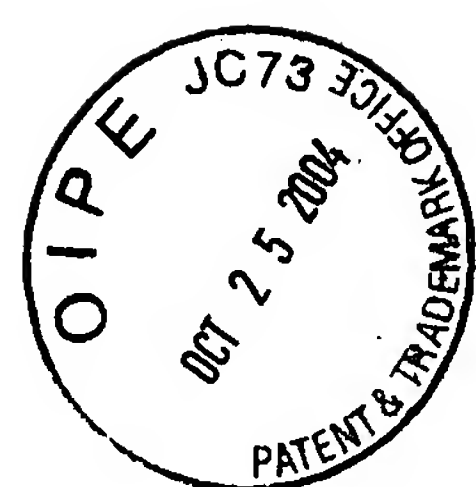


FIG. 26

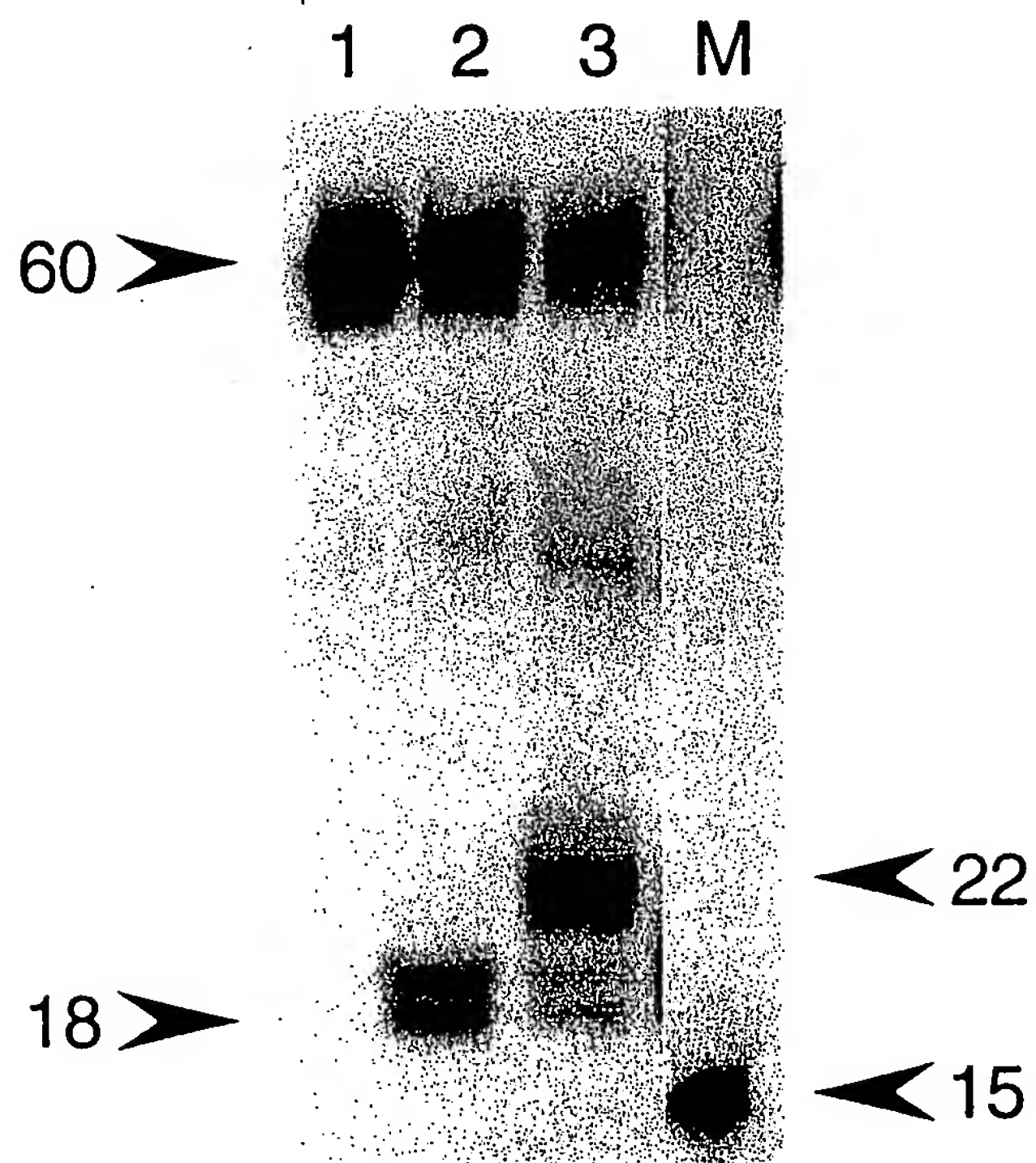
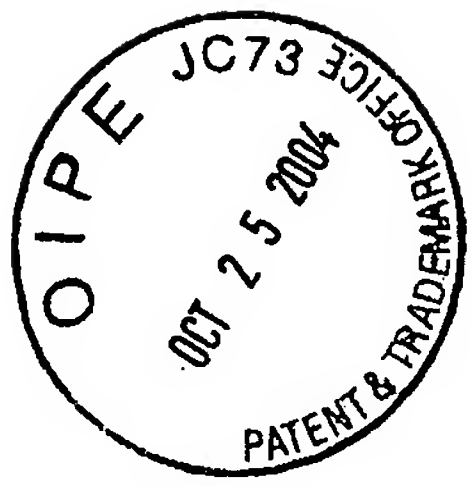


FIG. 27

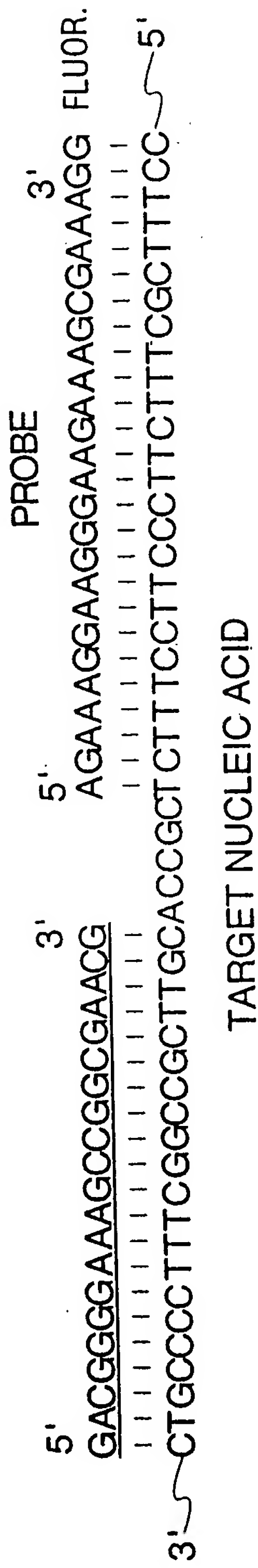
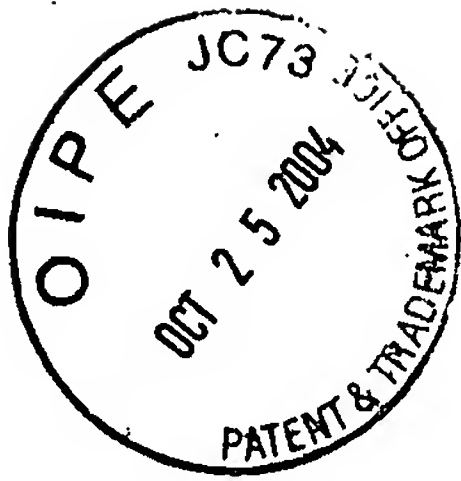


FIG. 28A

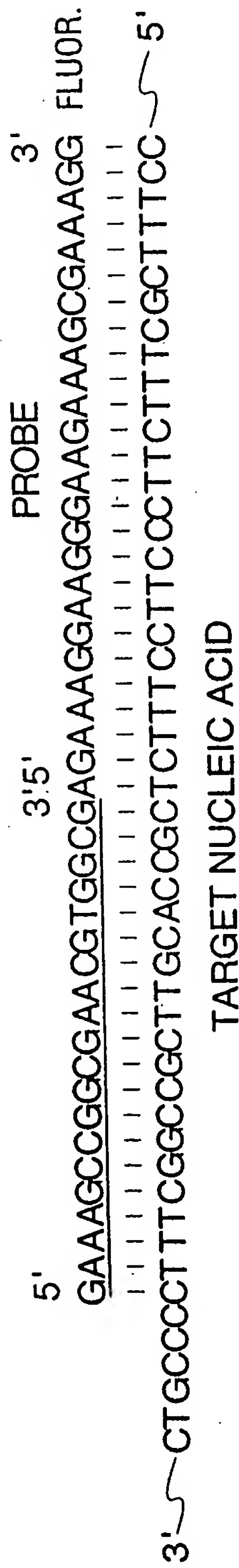


FIG. 28B

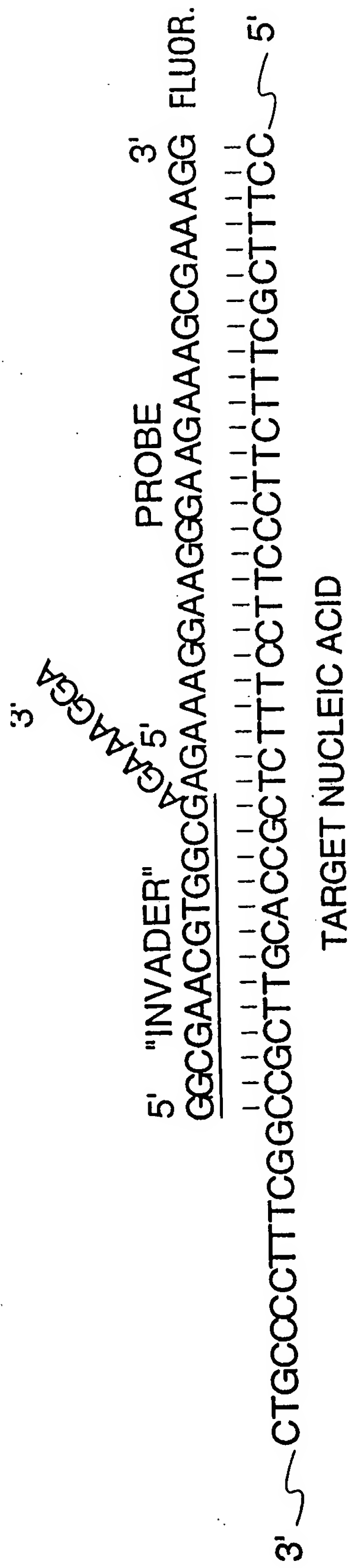


FIG. 28C

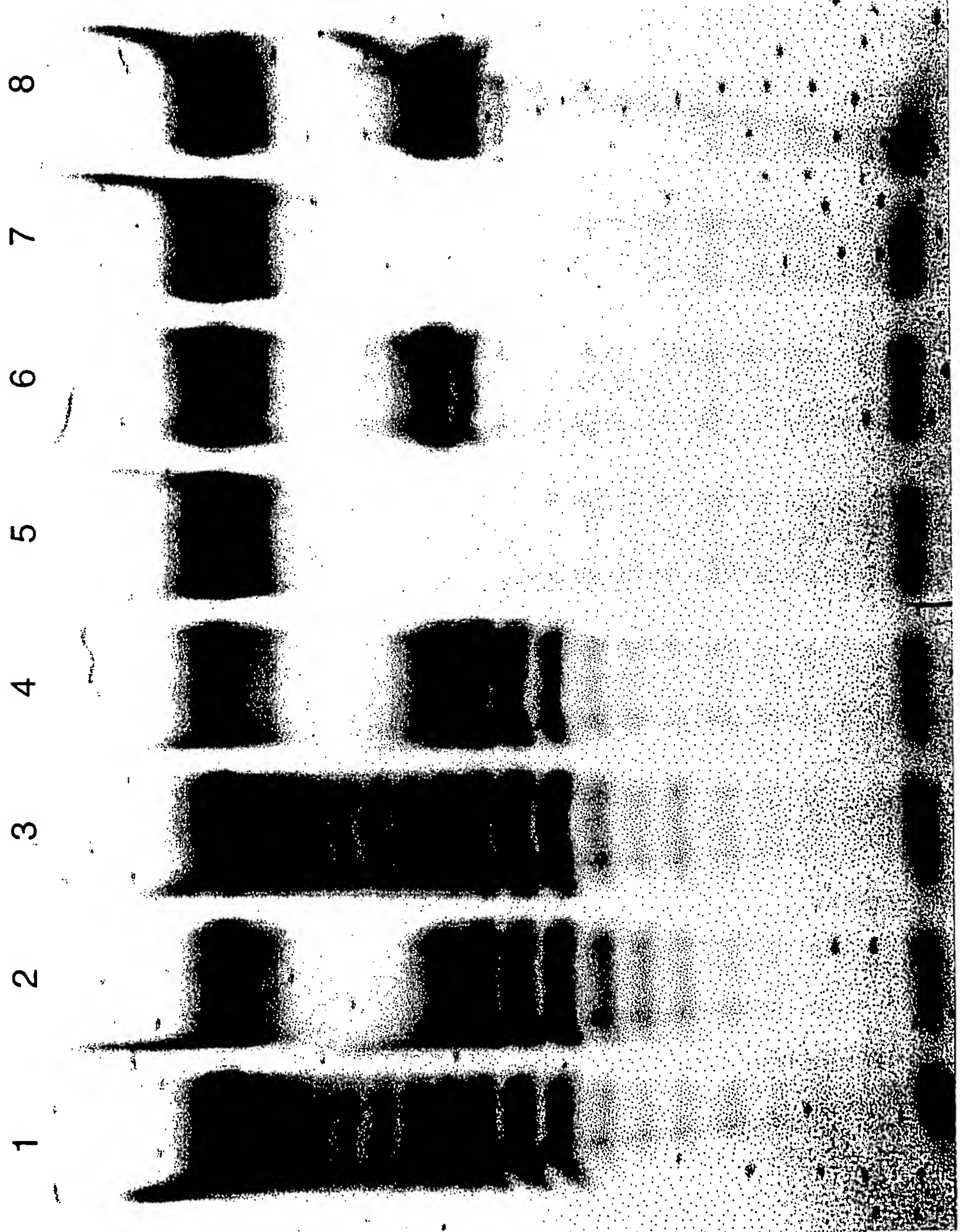
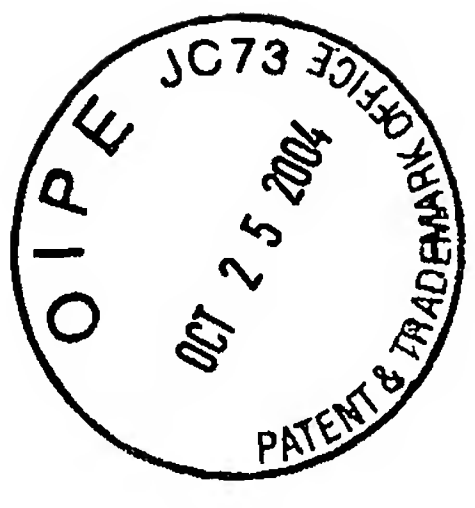


FIG. 29

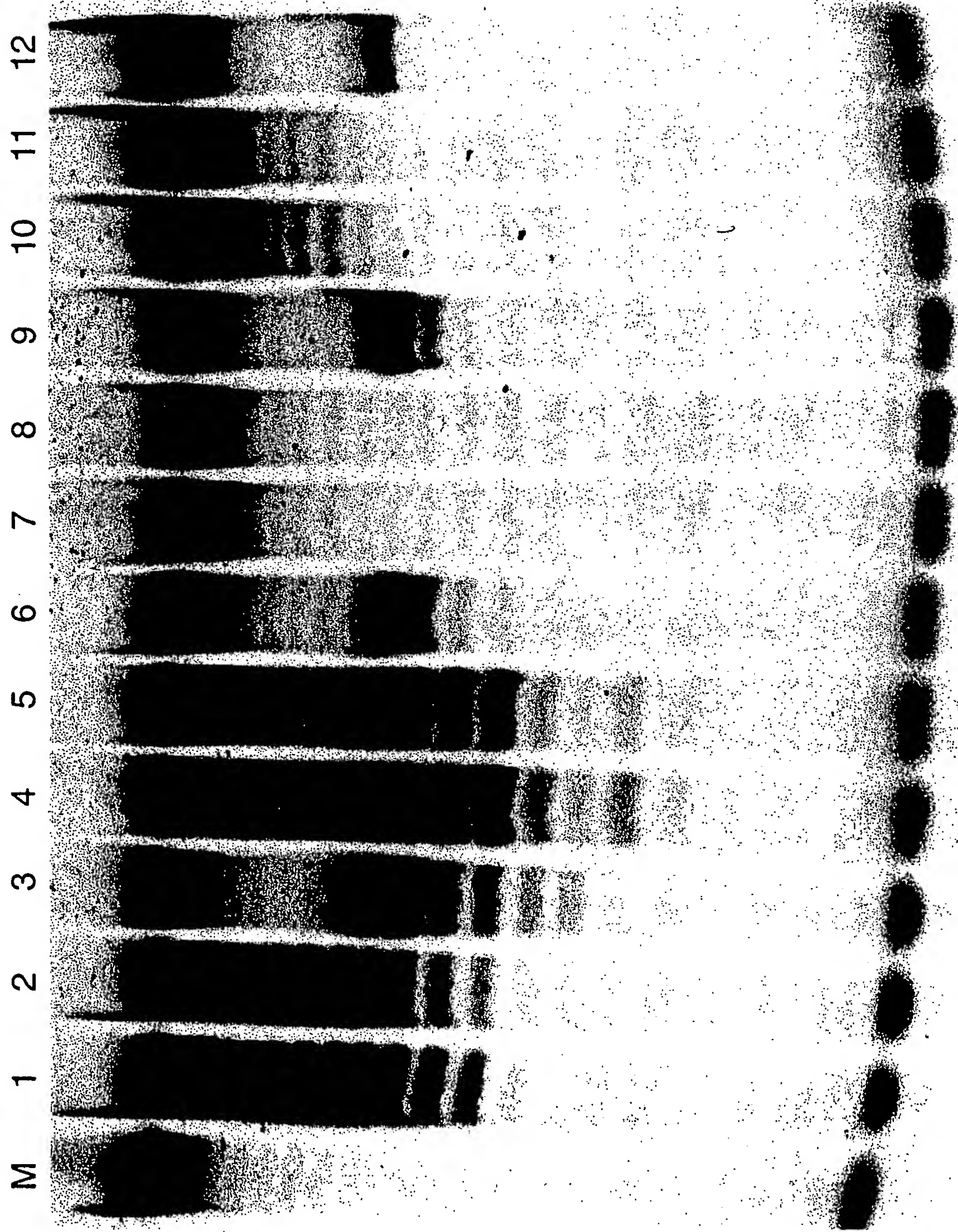
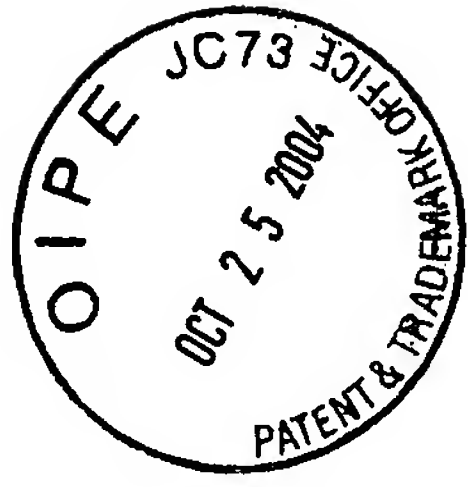


FIG. 30

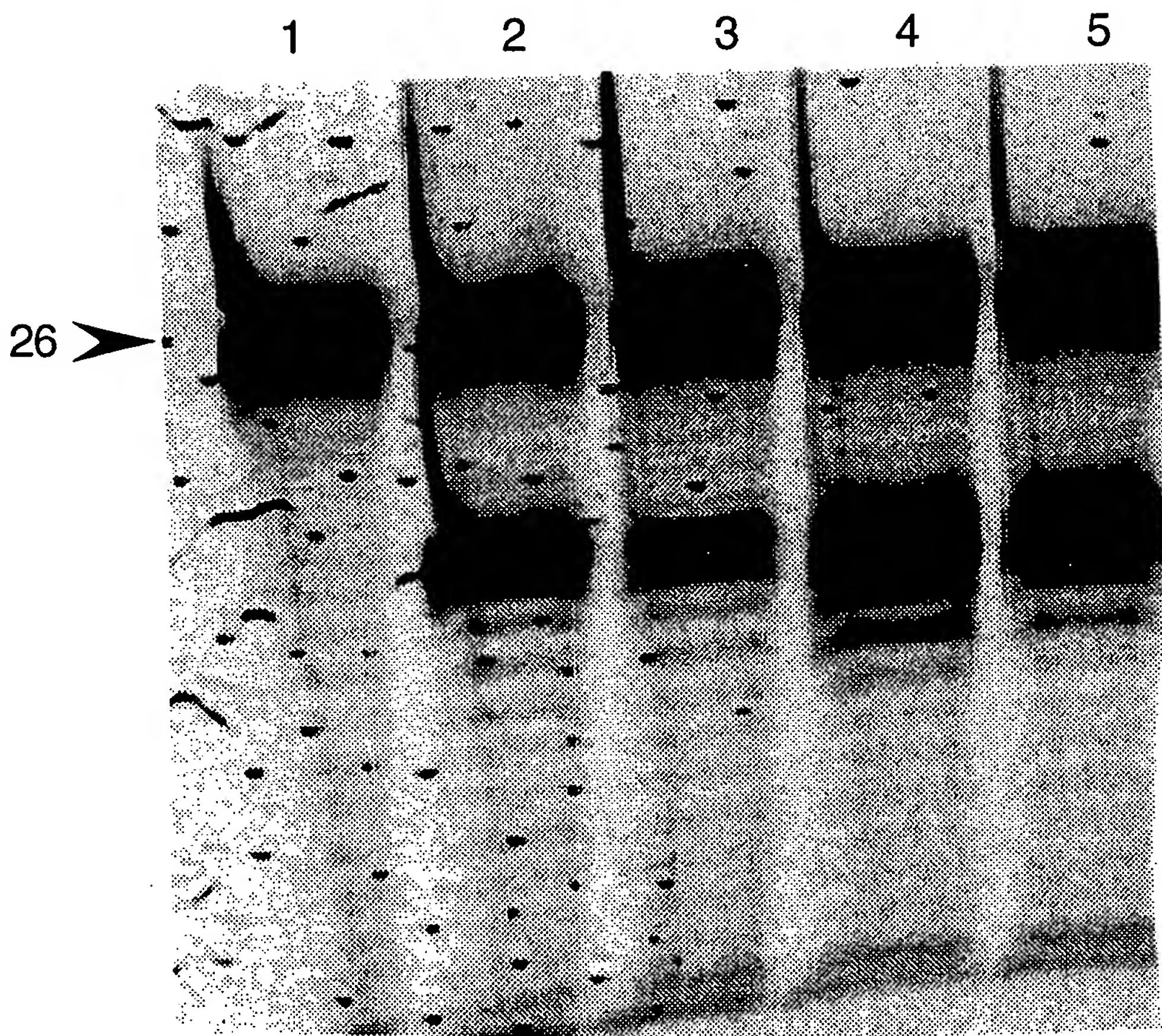


FIG. 31

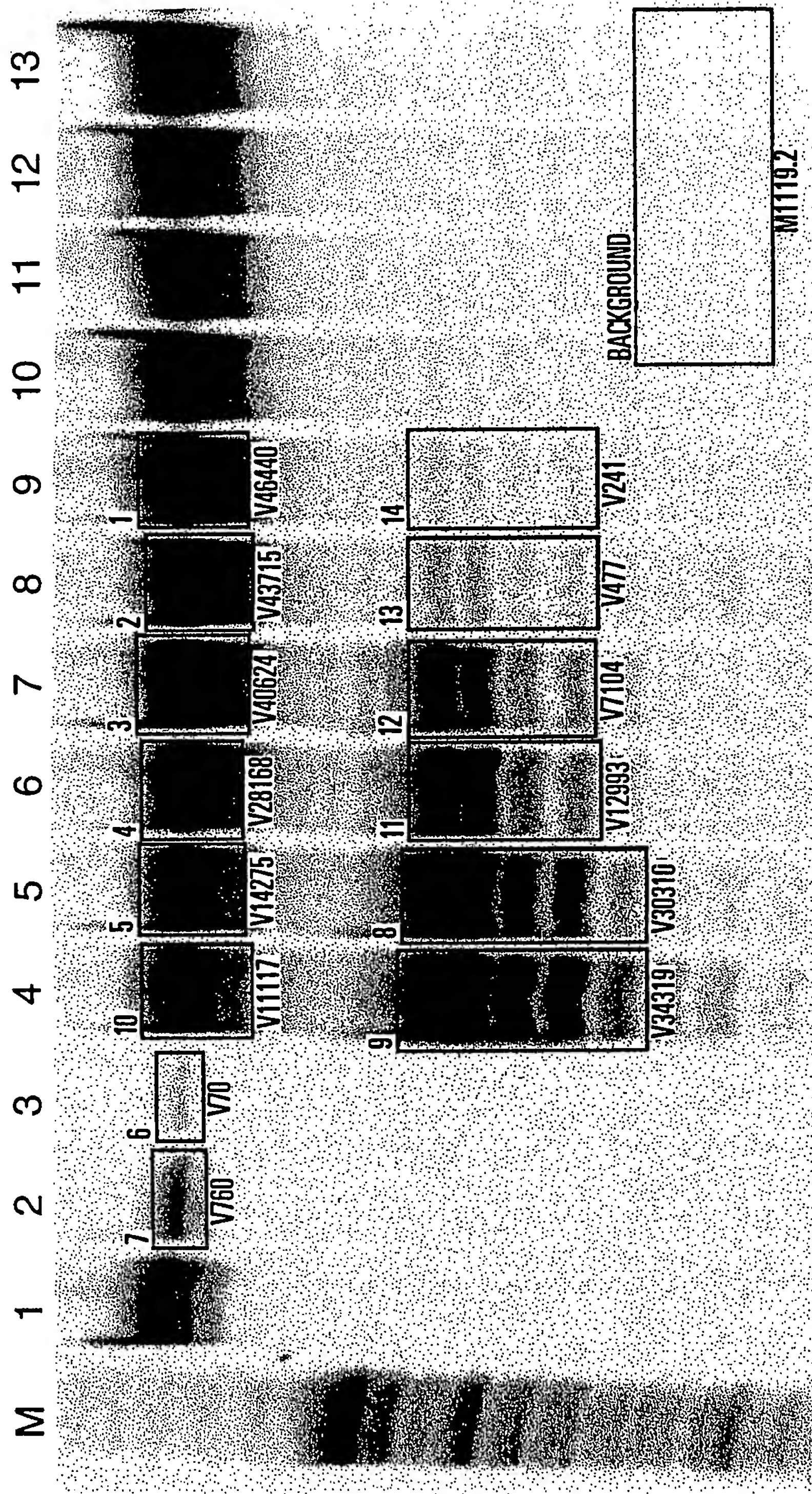


FIG. 32

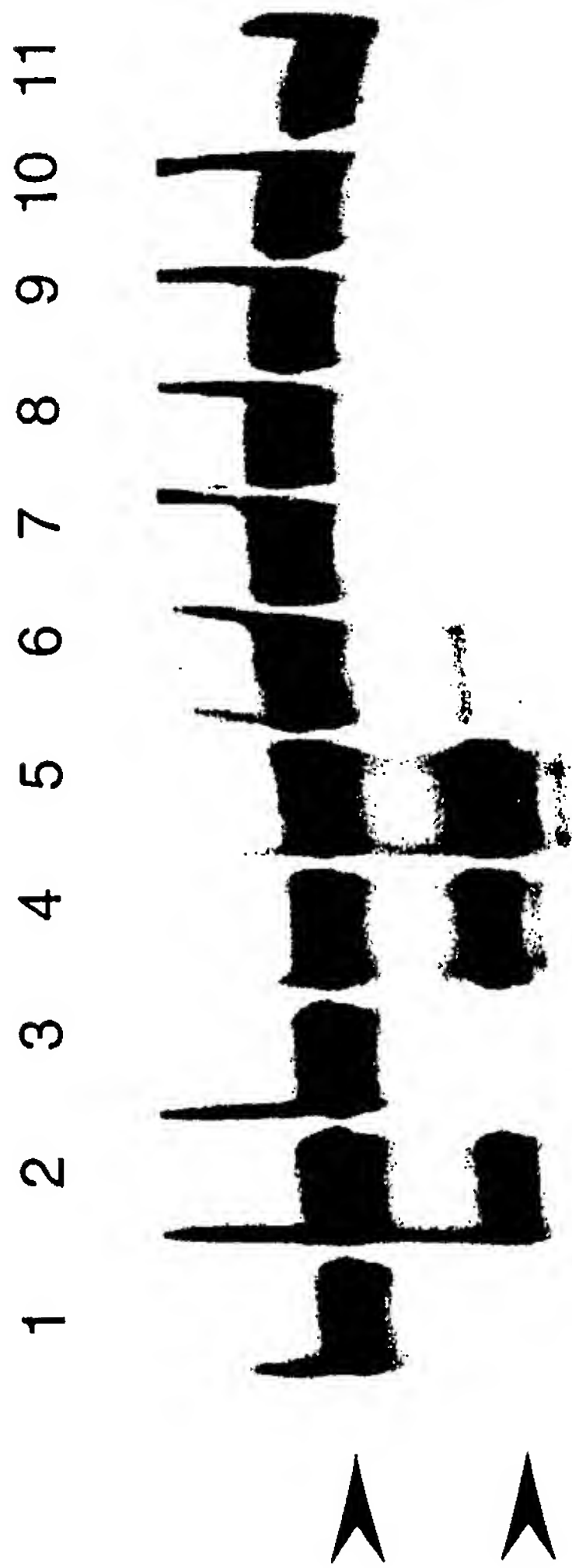
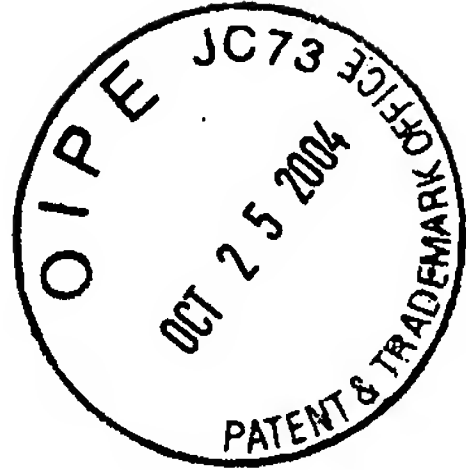


FIG. 33

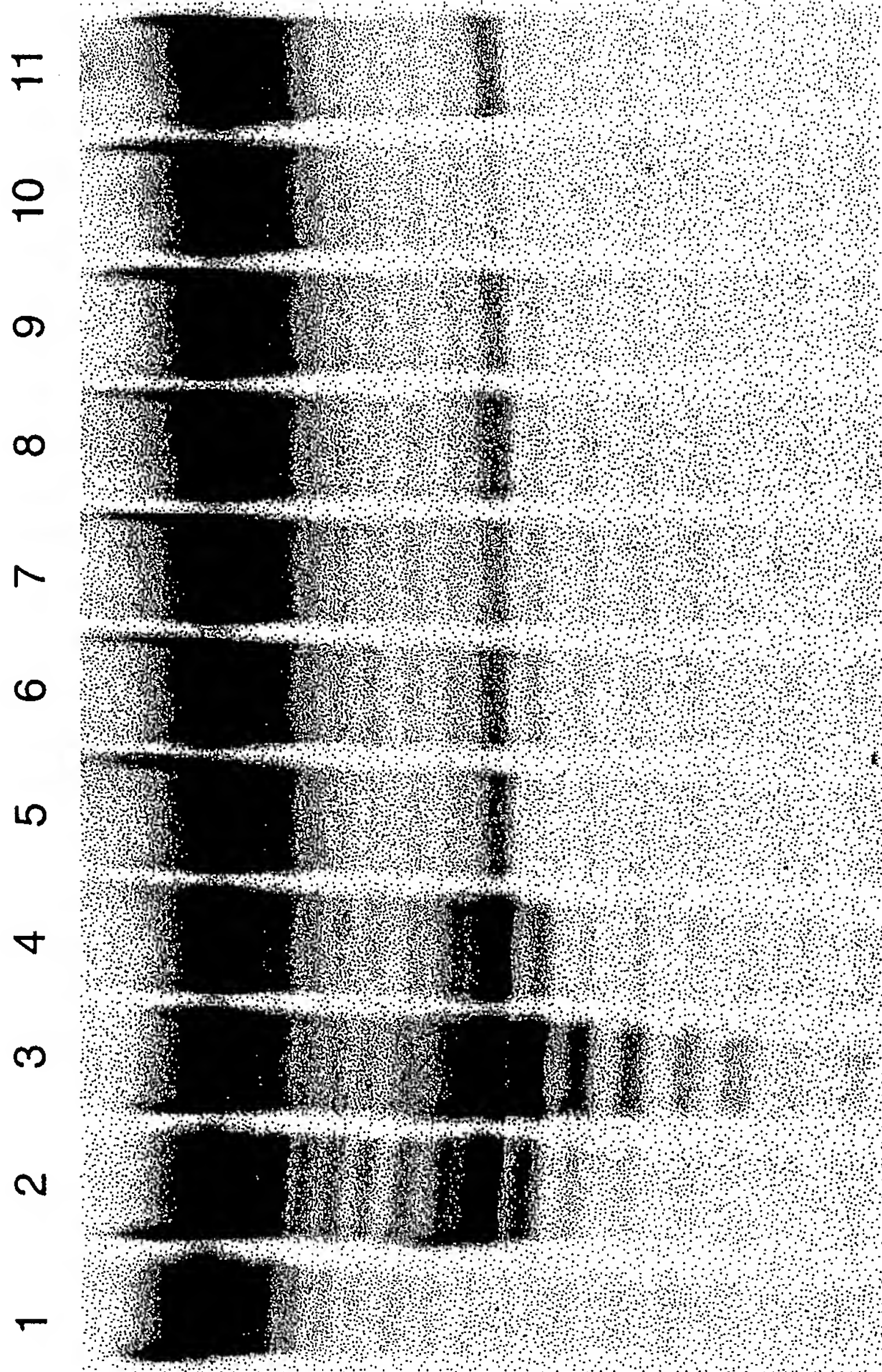
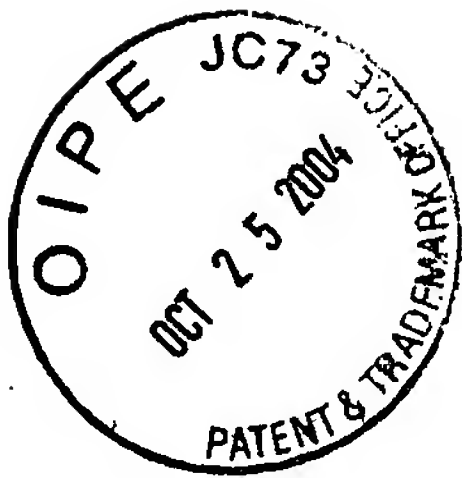


FIG. 34

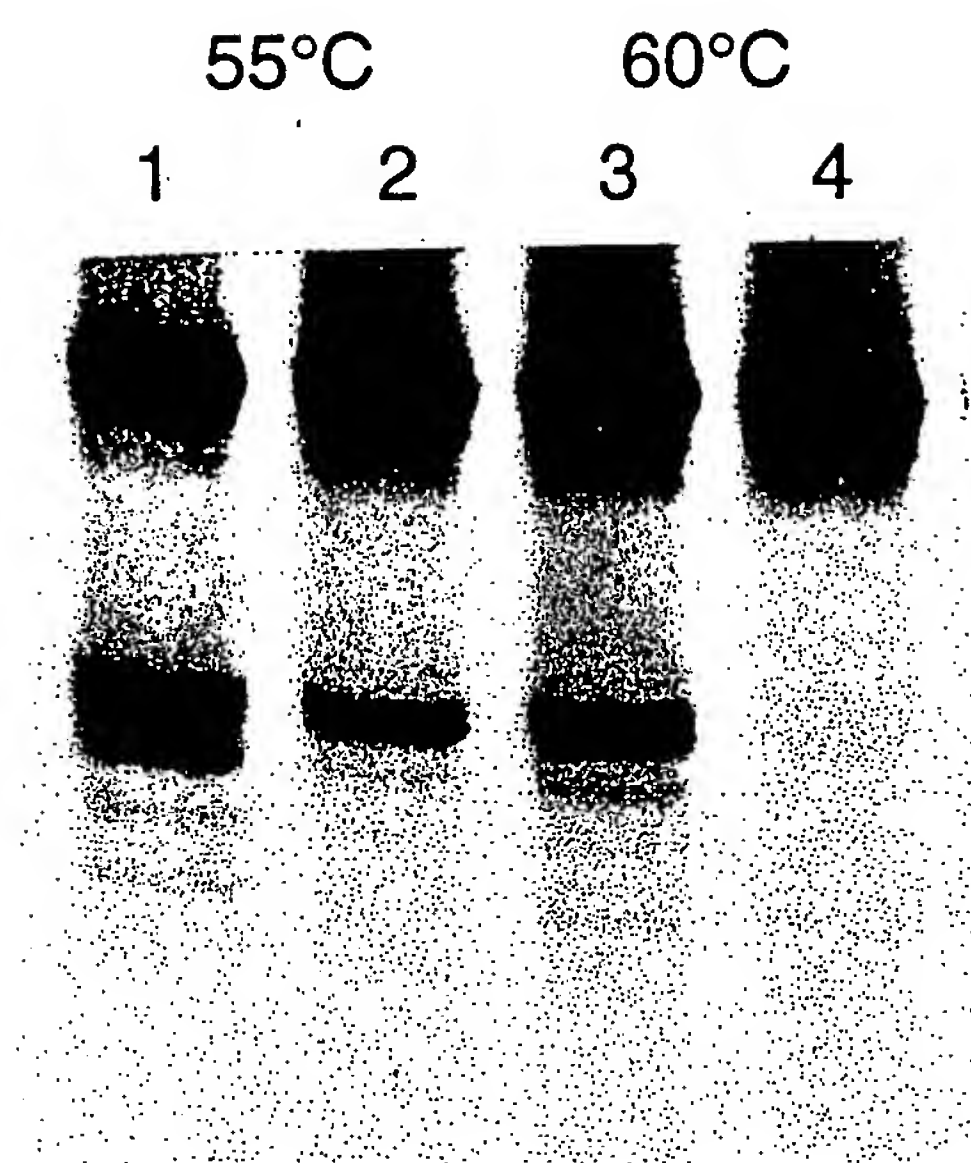
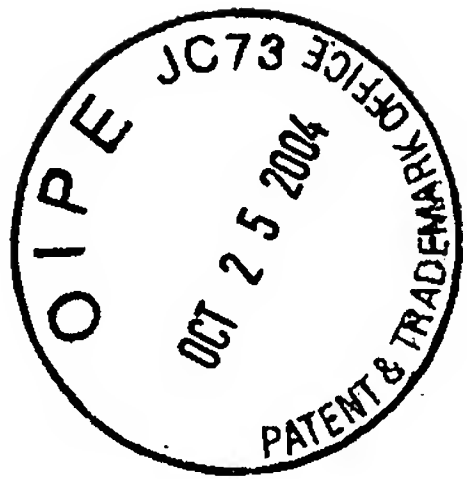


FIG. 35

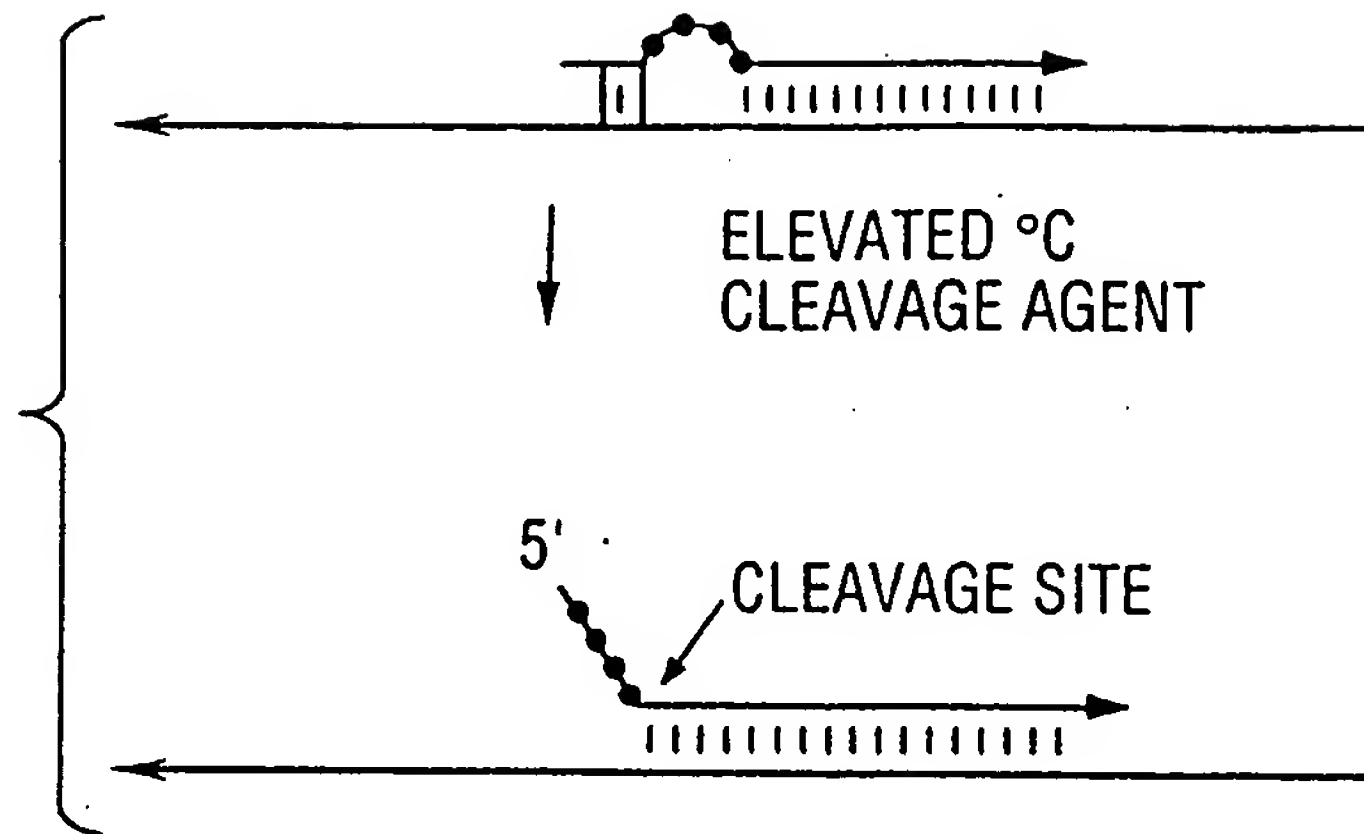


FIG. 36A

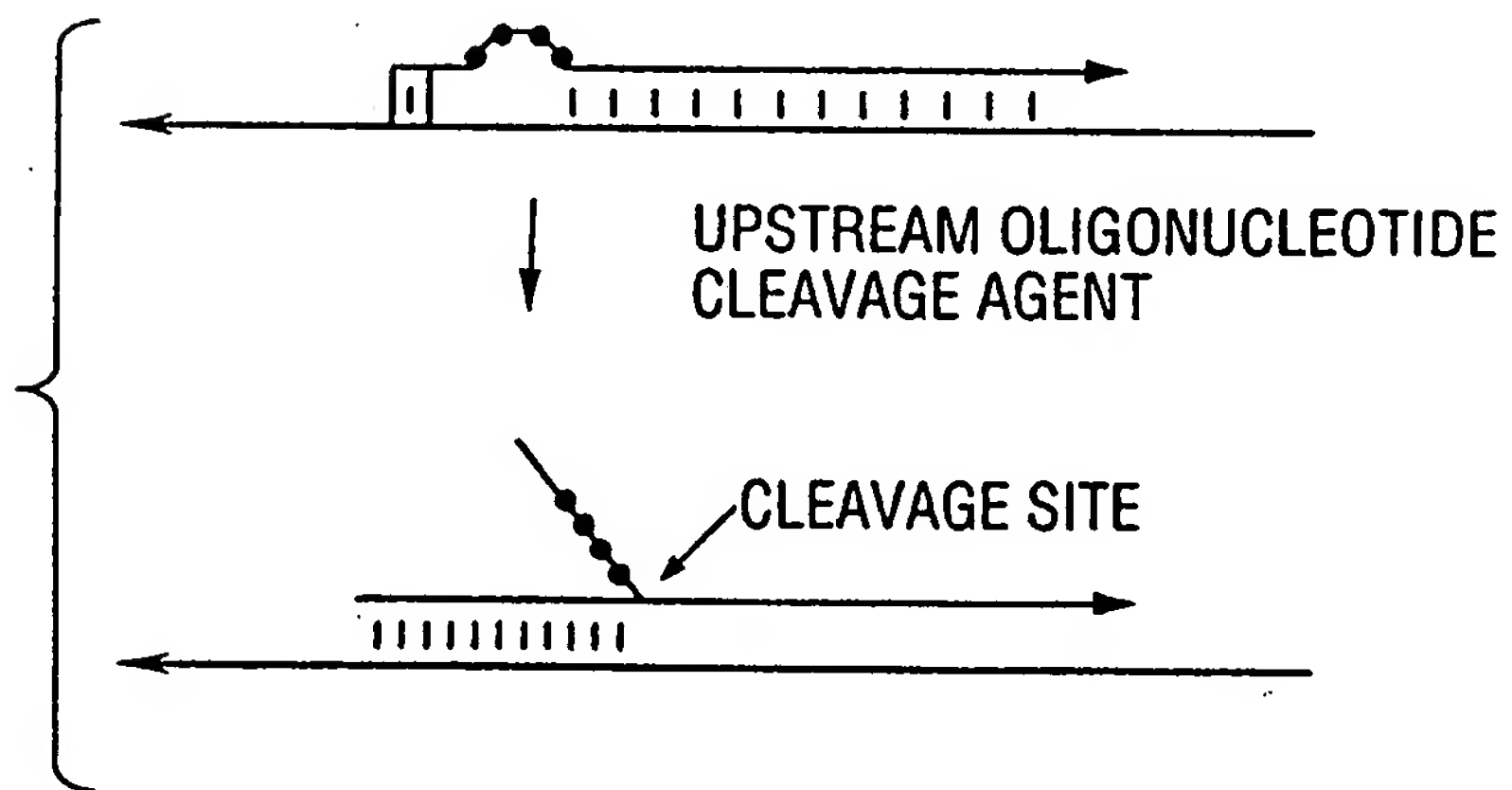


FIG. 36B

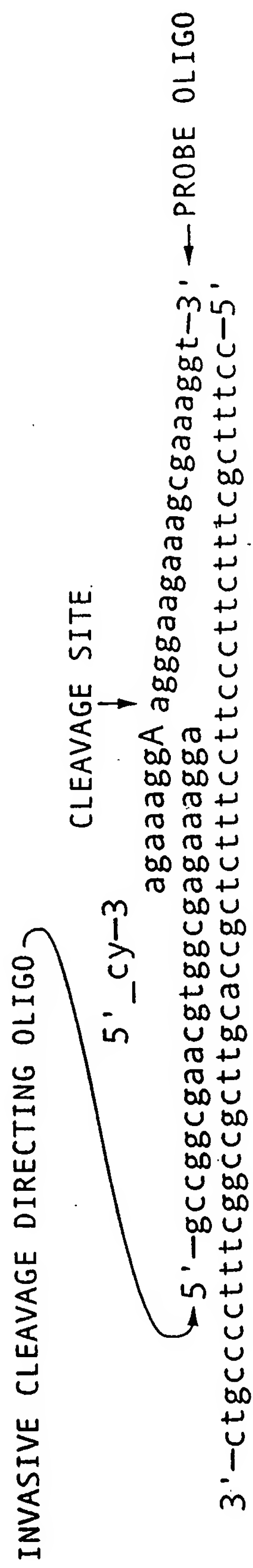
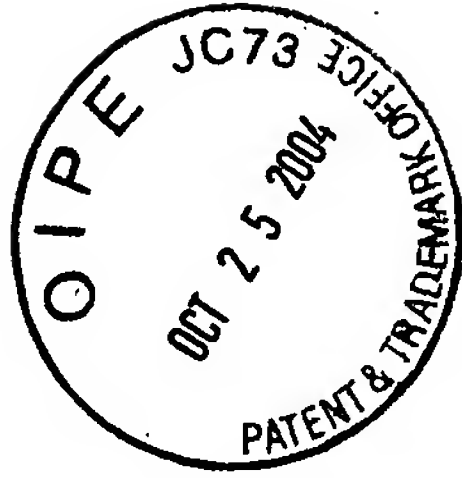


FIG. 37

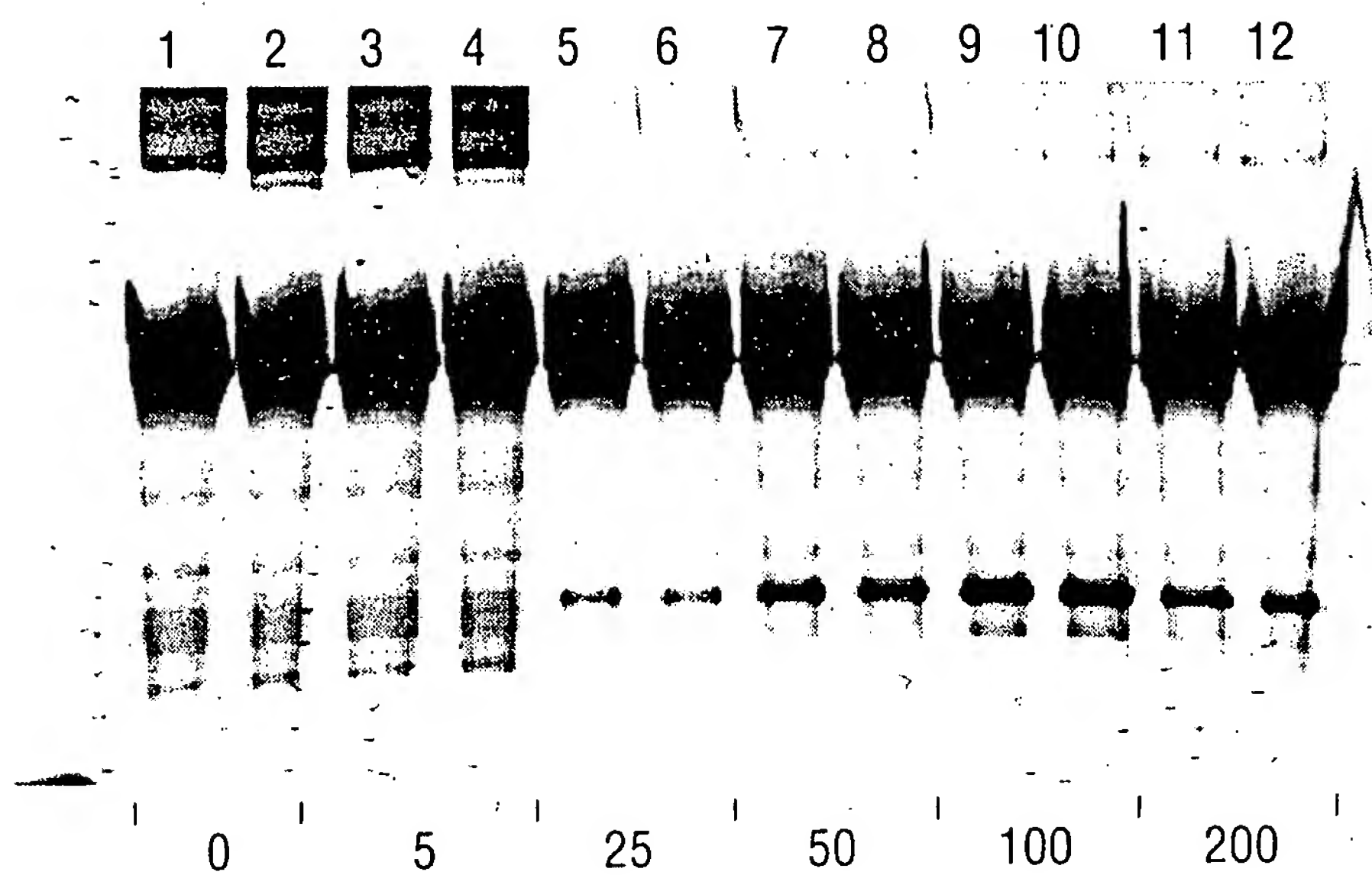
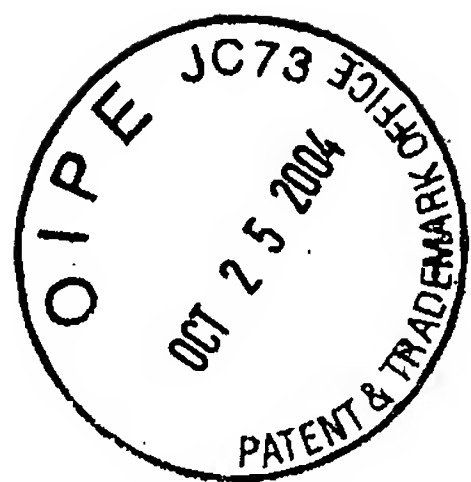


FIG. 38

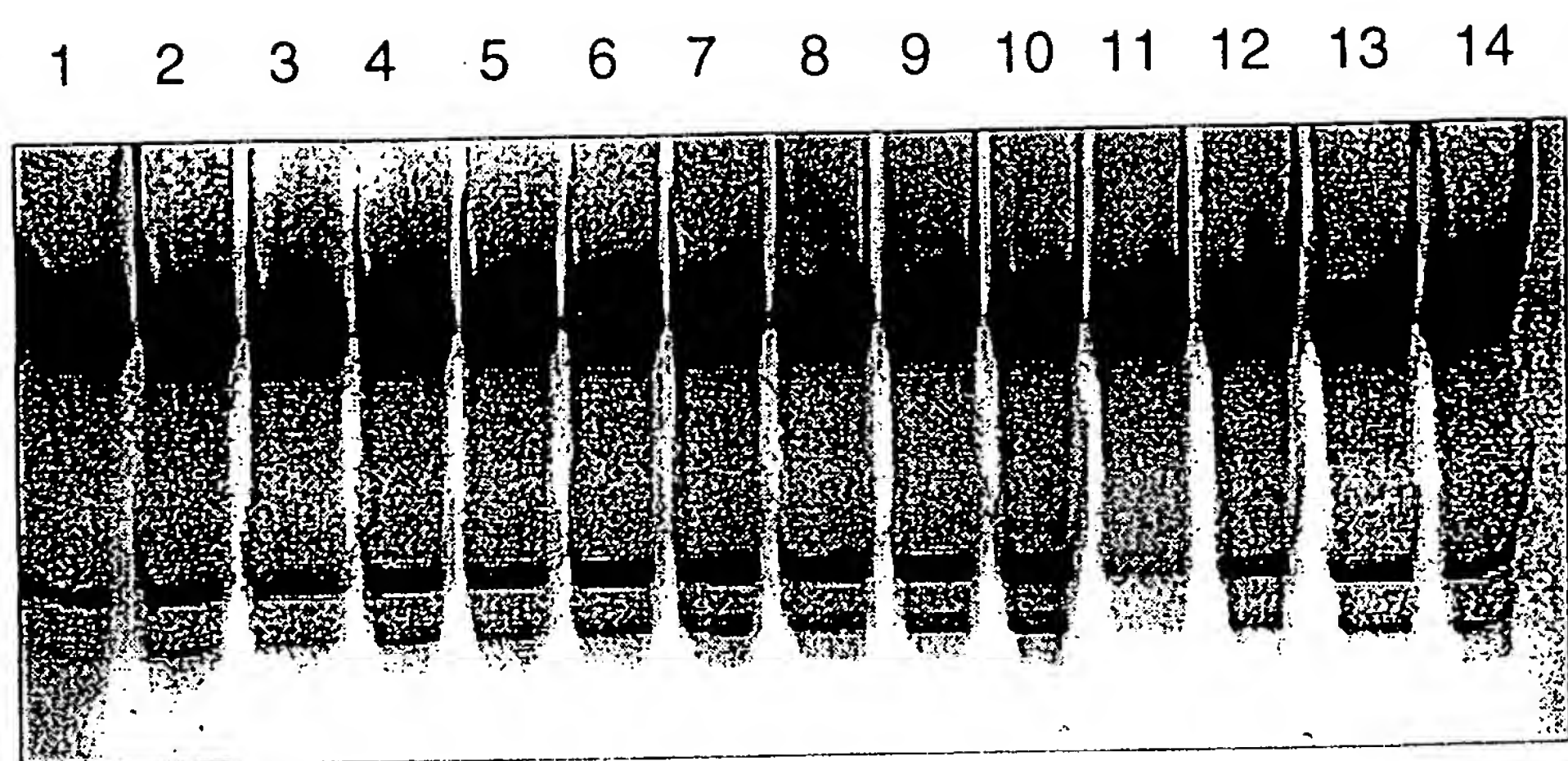
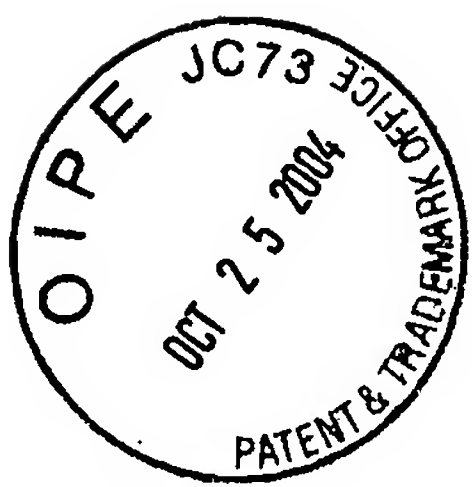


FIG. 39

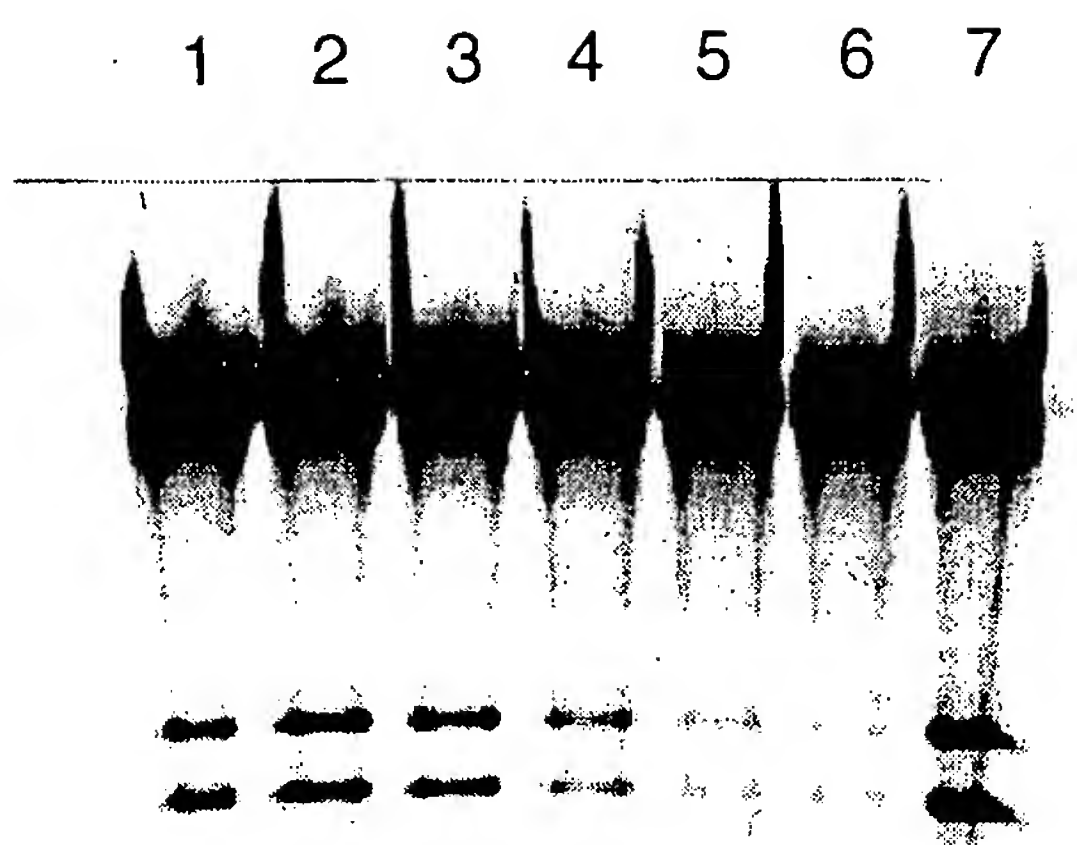
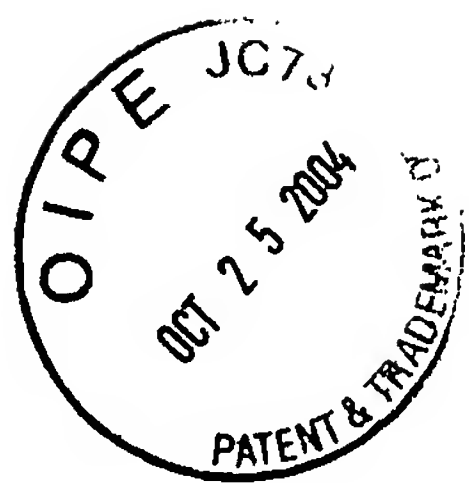


FIG. 40

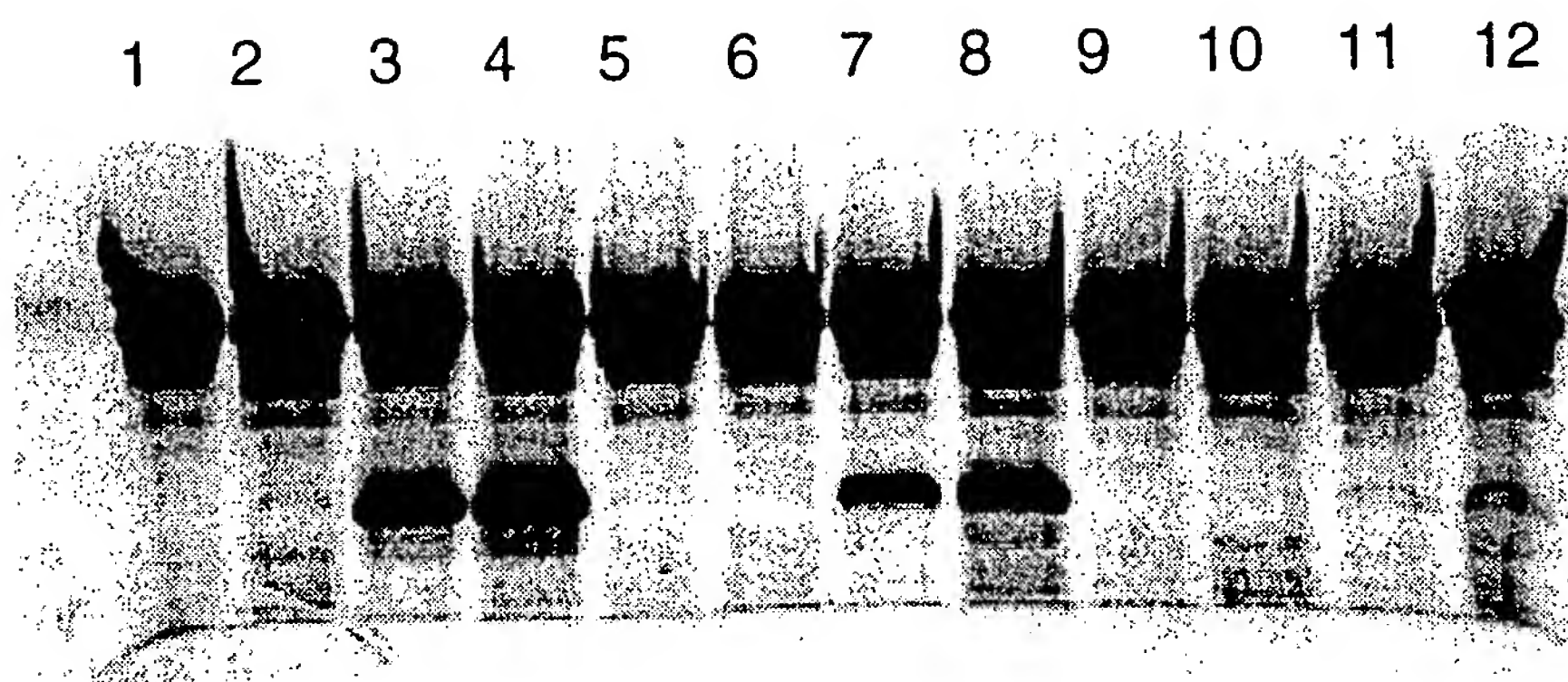
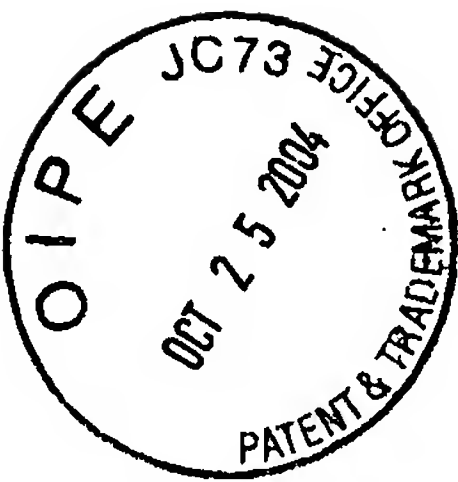


FIG. 41

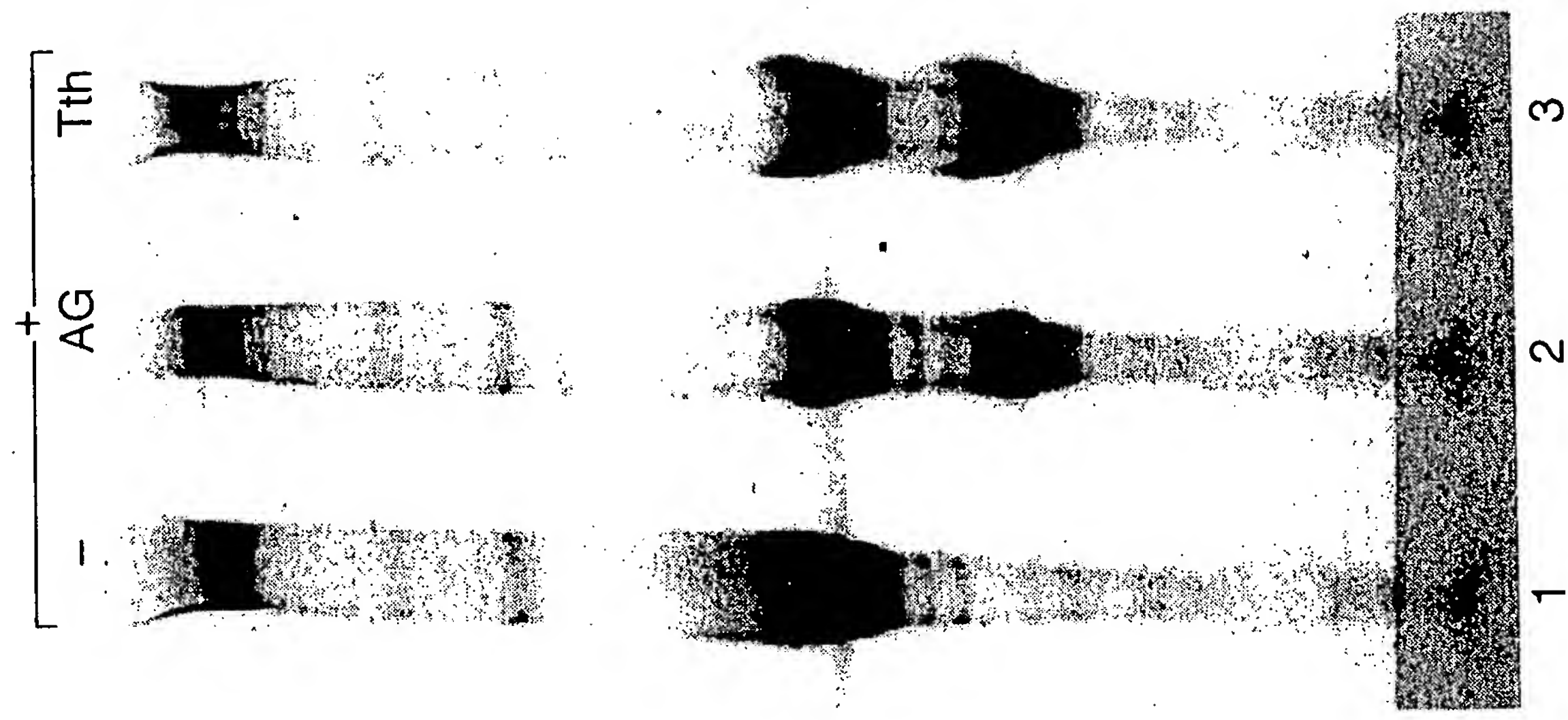


FIG. 42B

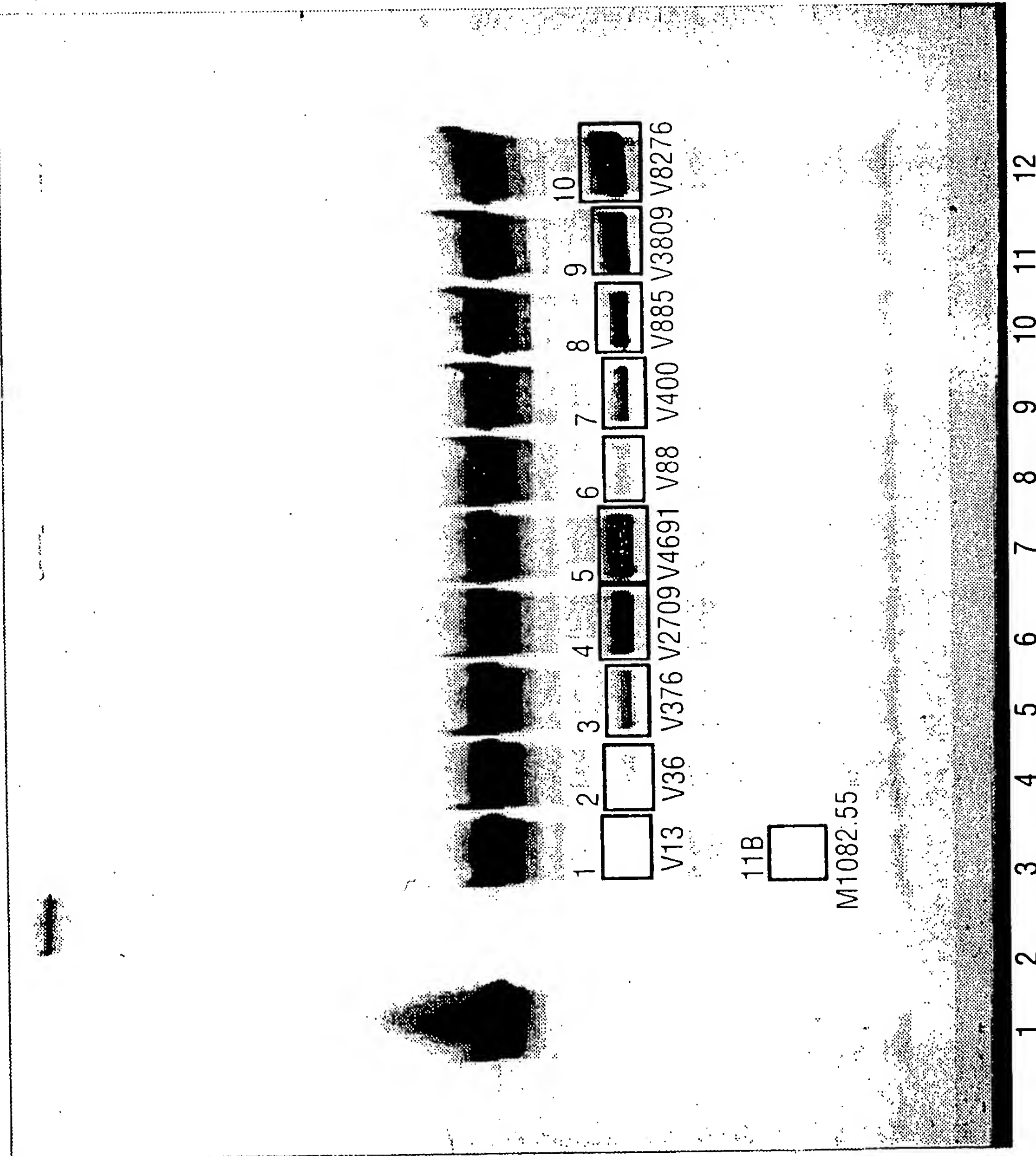


TARGET RNA —

UNCLEAVED
PROBE —

CLEAVED
PROBE —

FIG. 42A



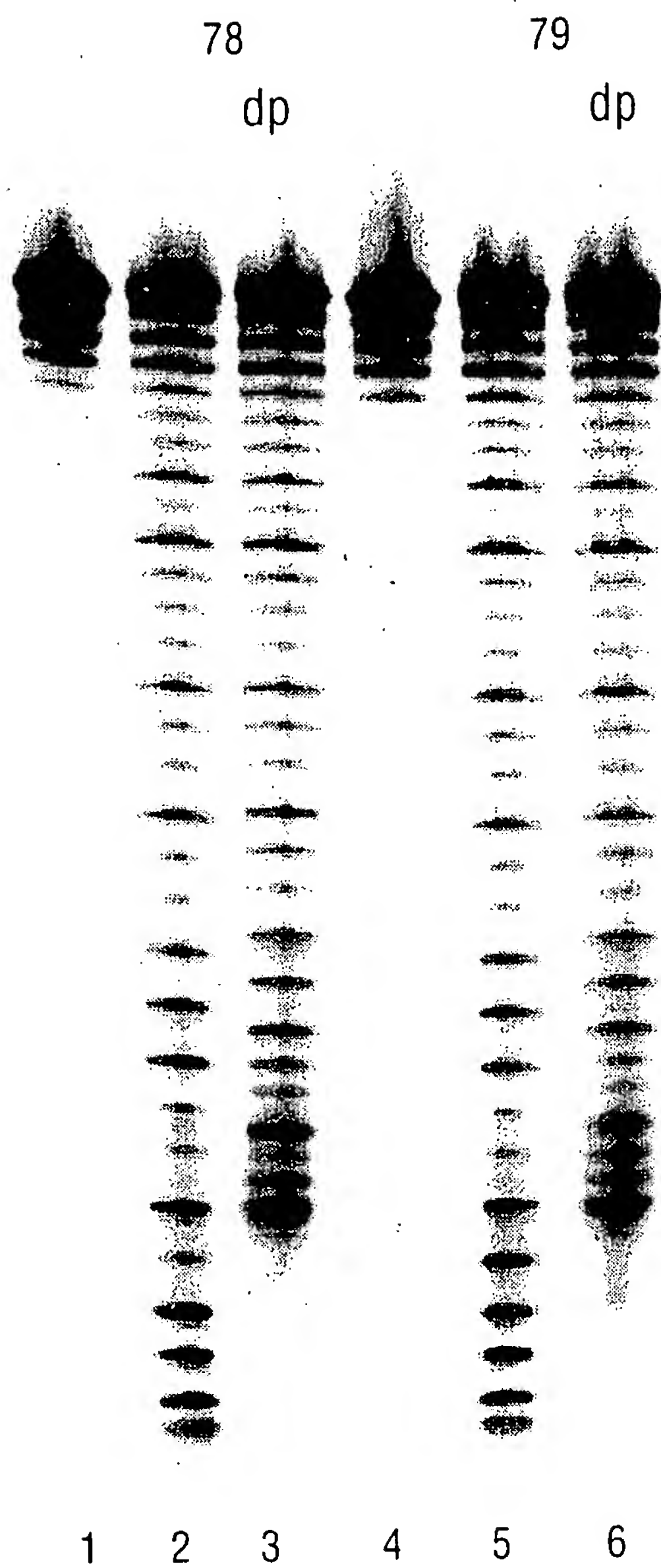
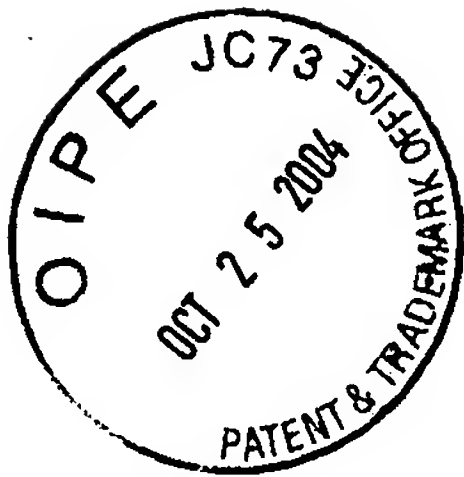


FIG. 44

70 (C10 amino T's)
74 (C6 amino T's)

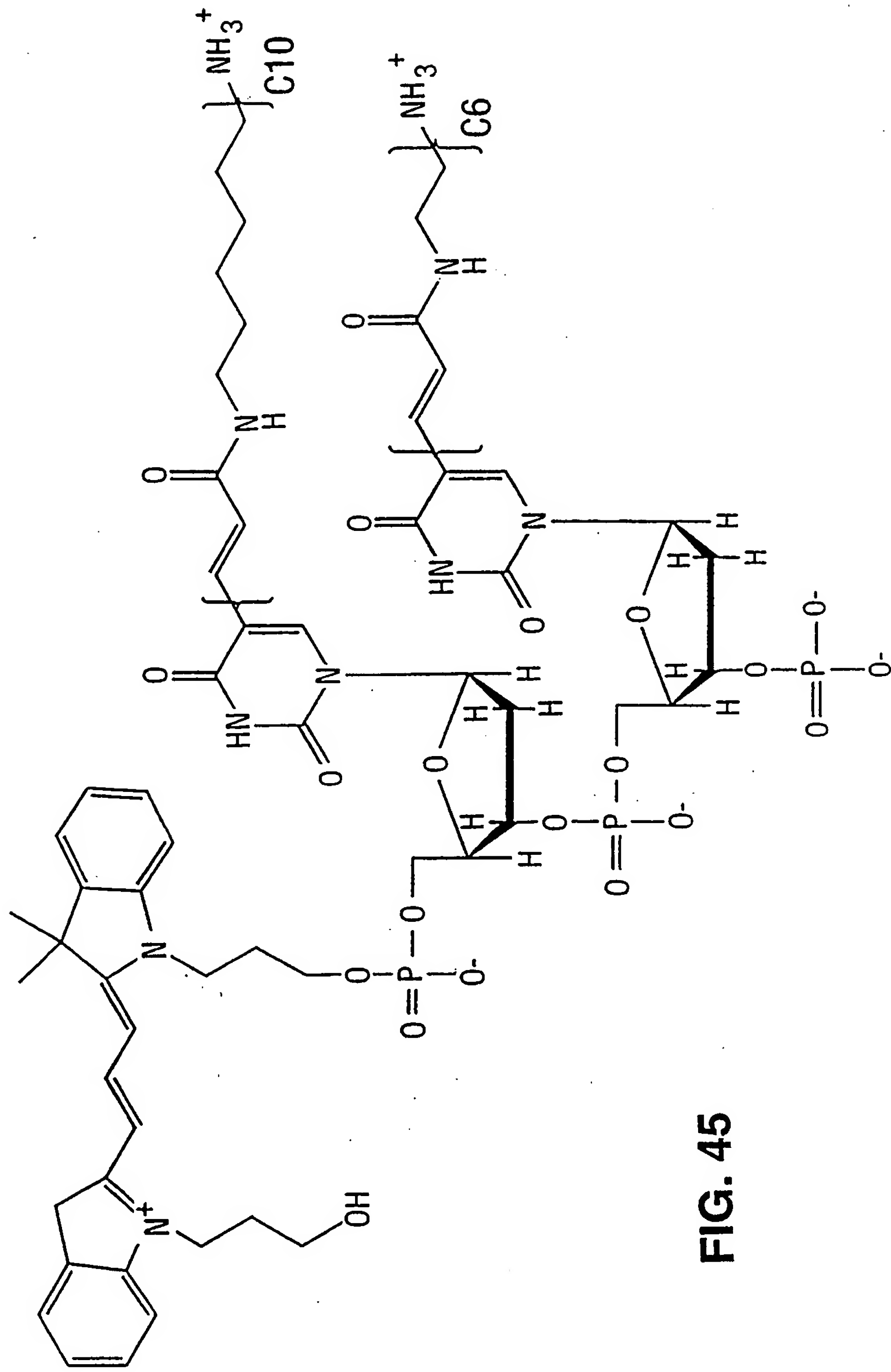


FIG. 45



76

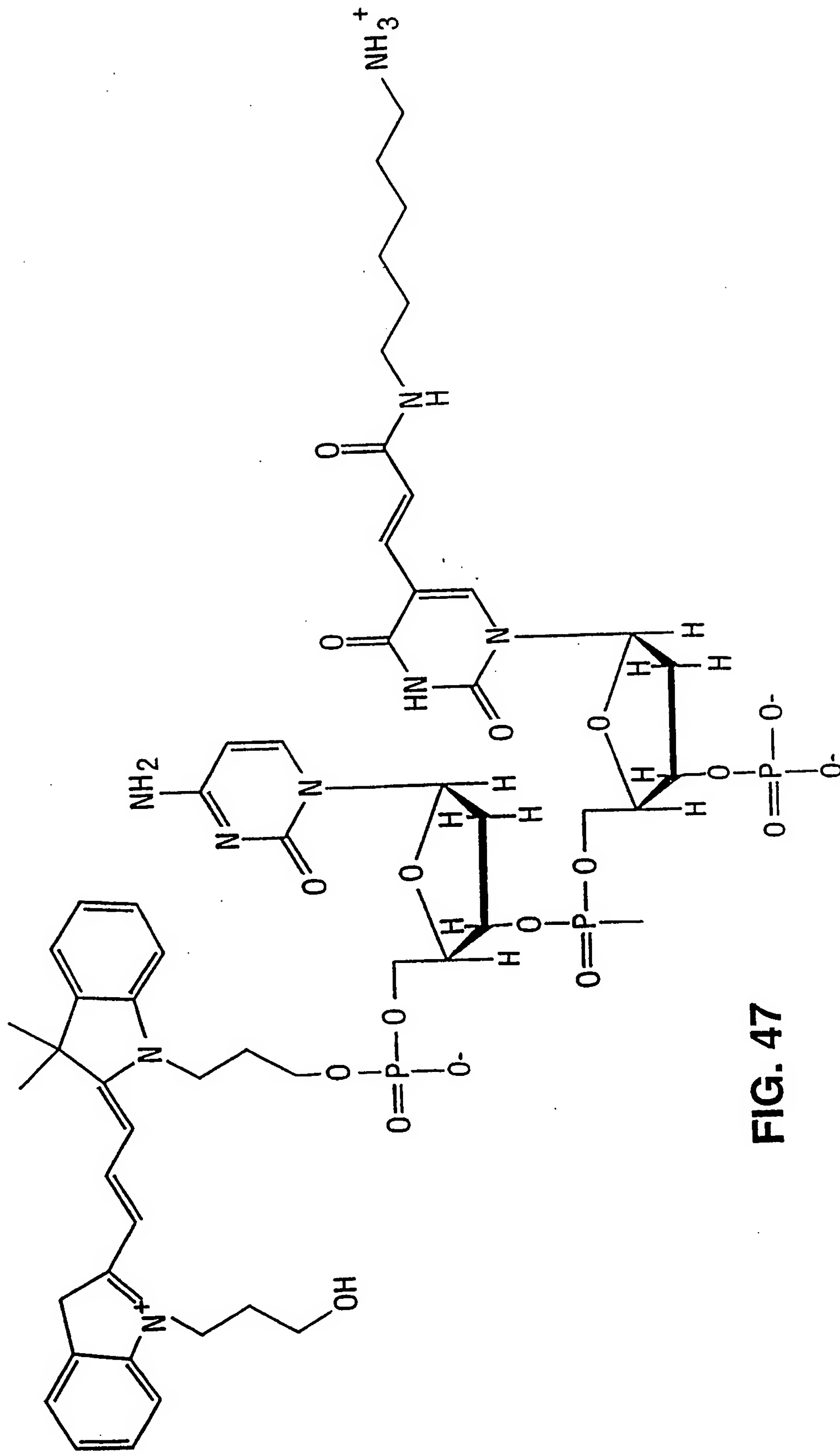


FIG. 47

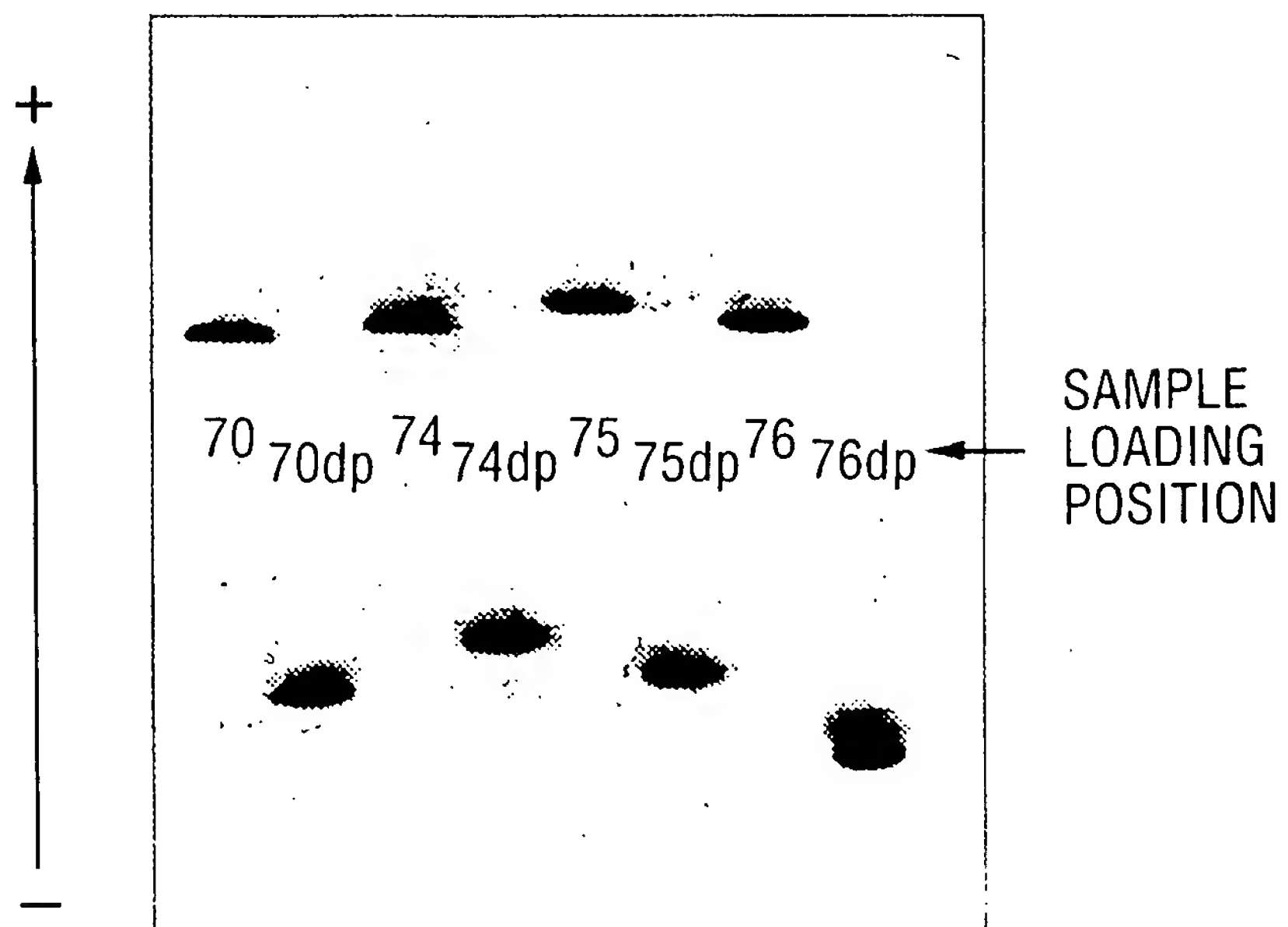
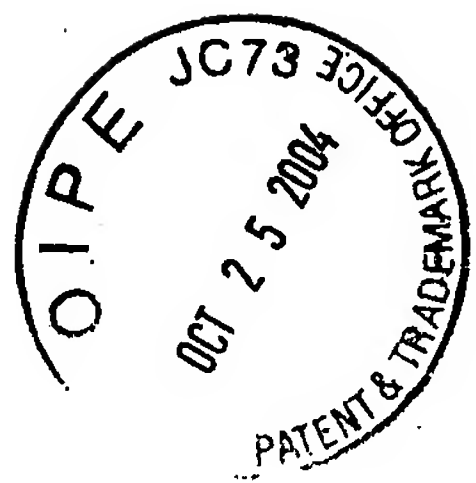


FIG. 48

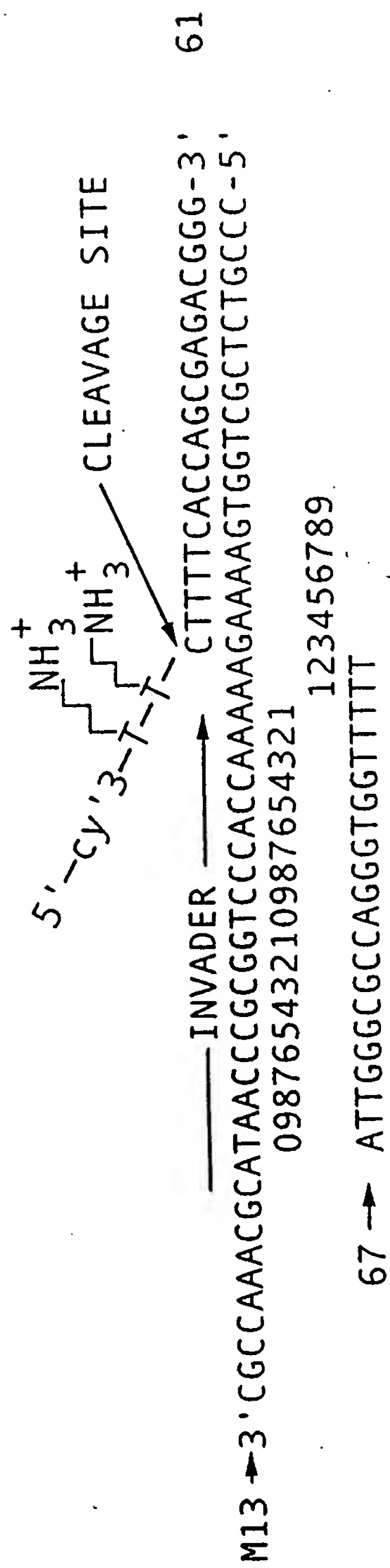
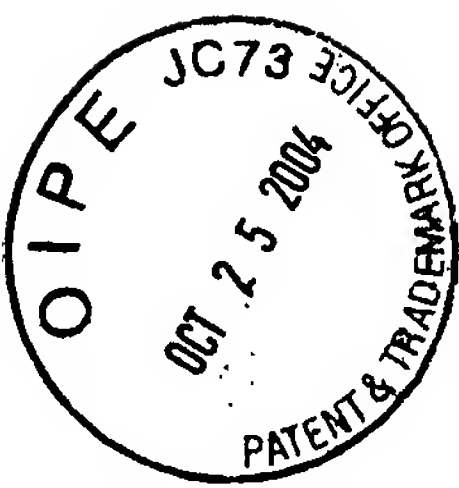


FIG. 49A

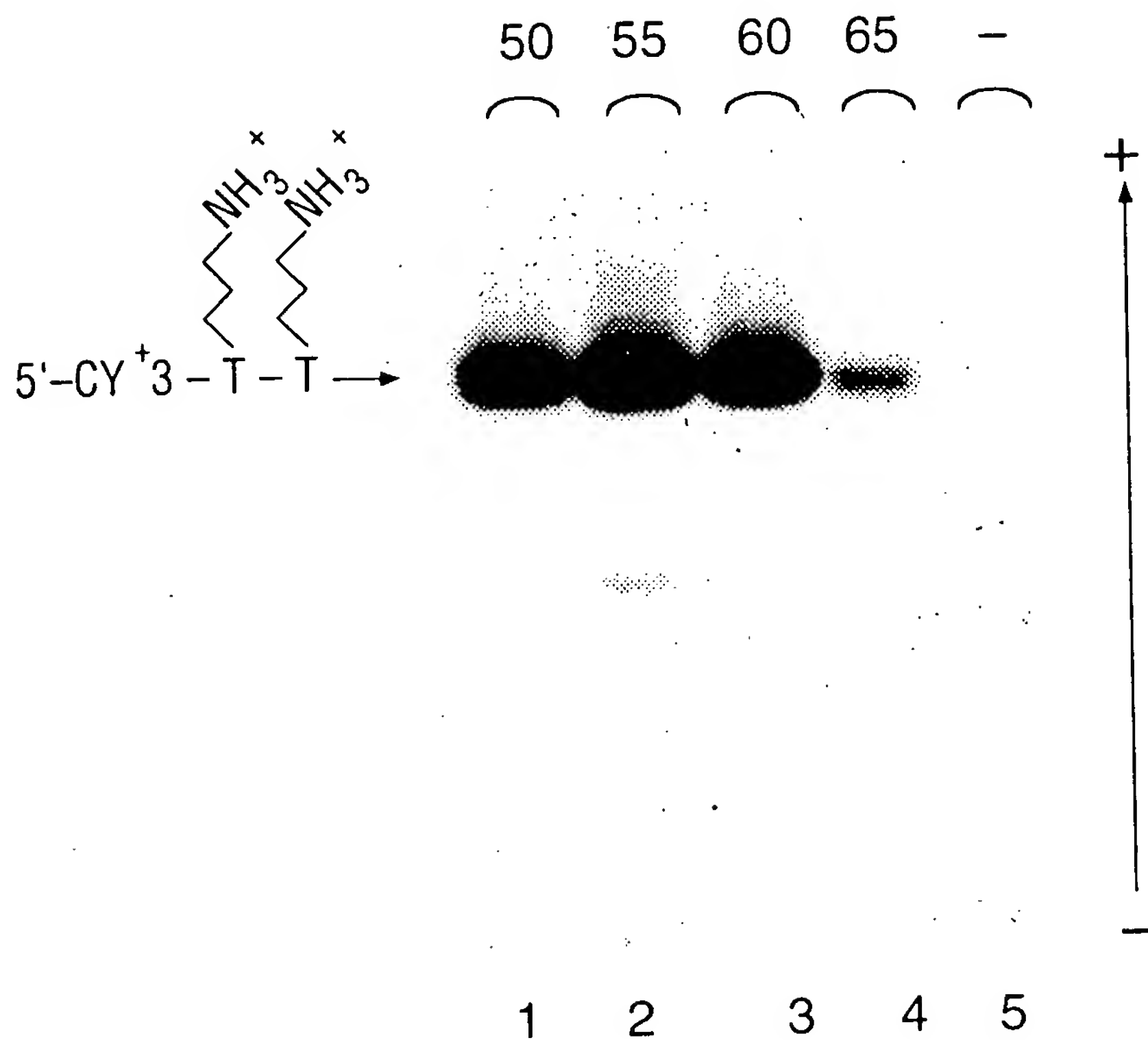
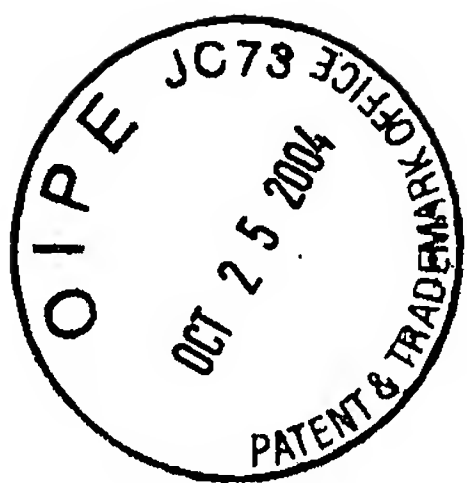


FIG. 49B

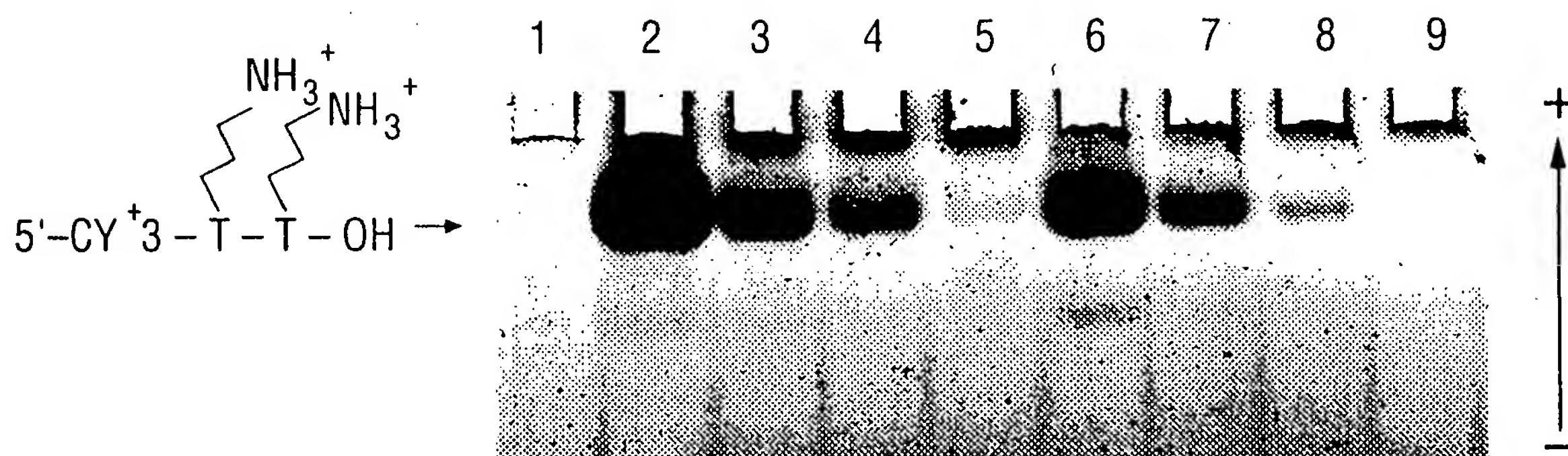
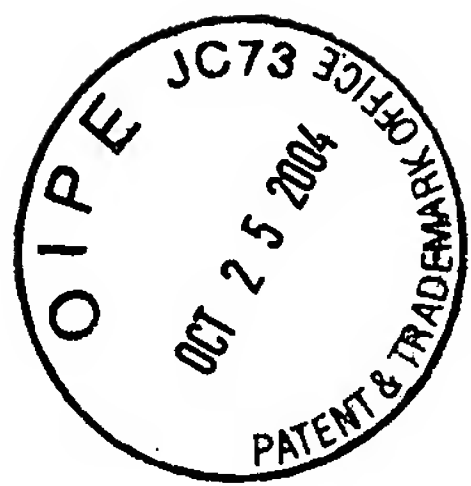


FIG. 50

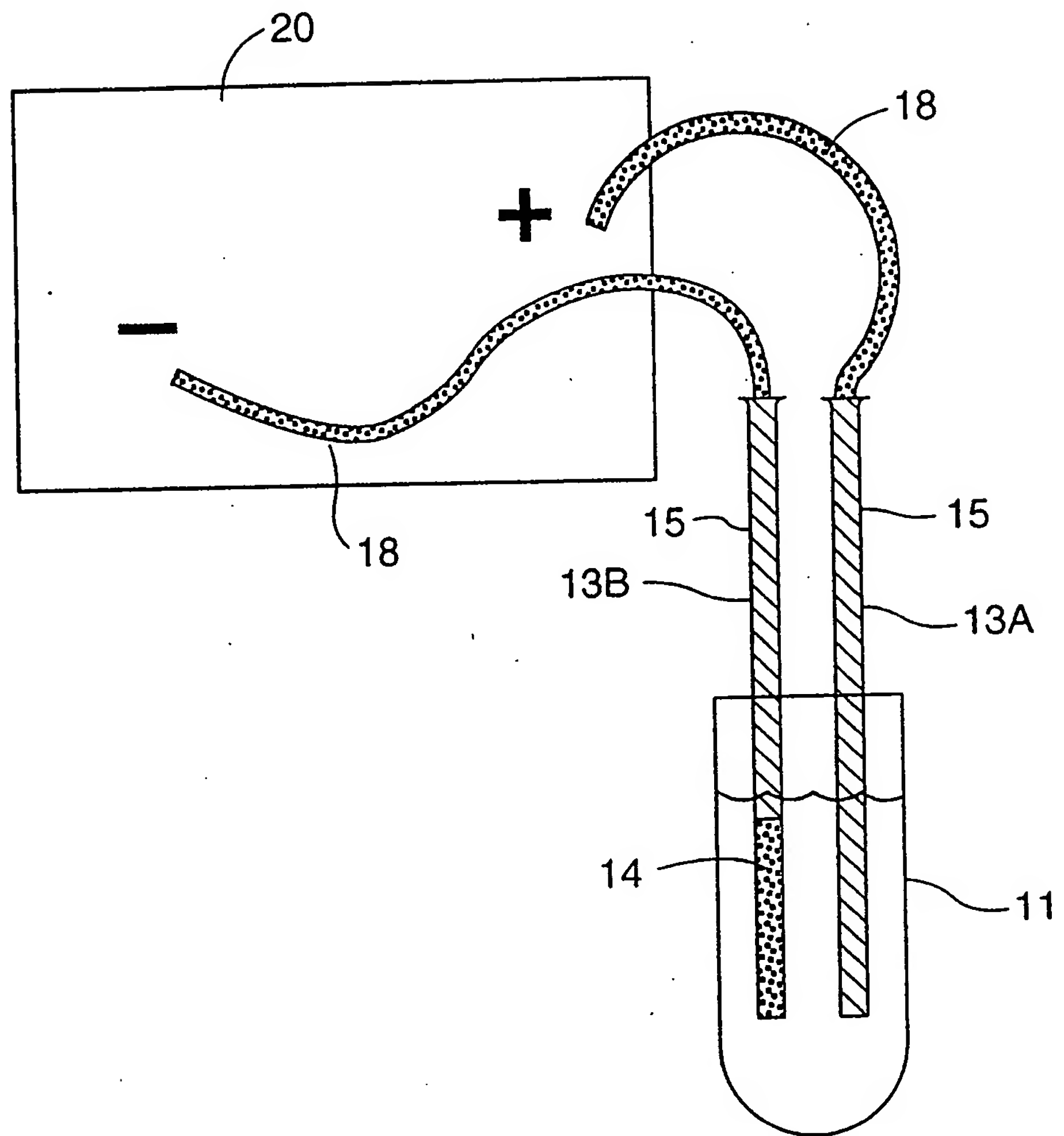
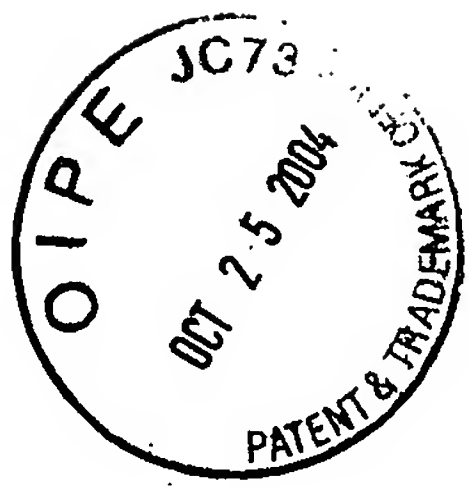


FIG. 51

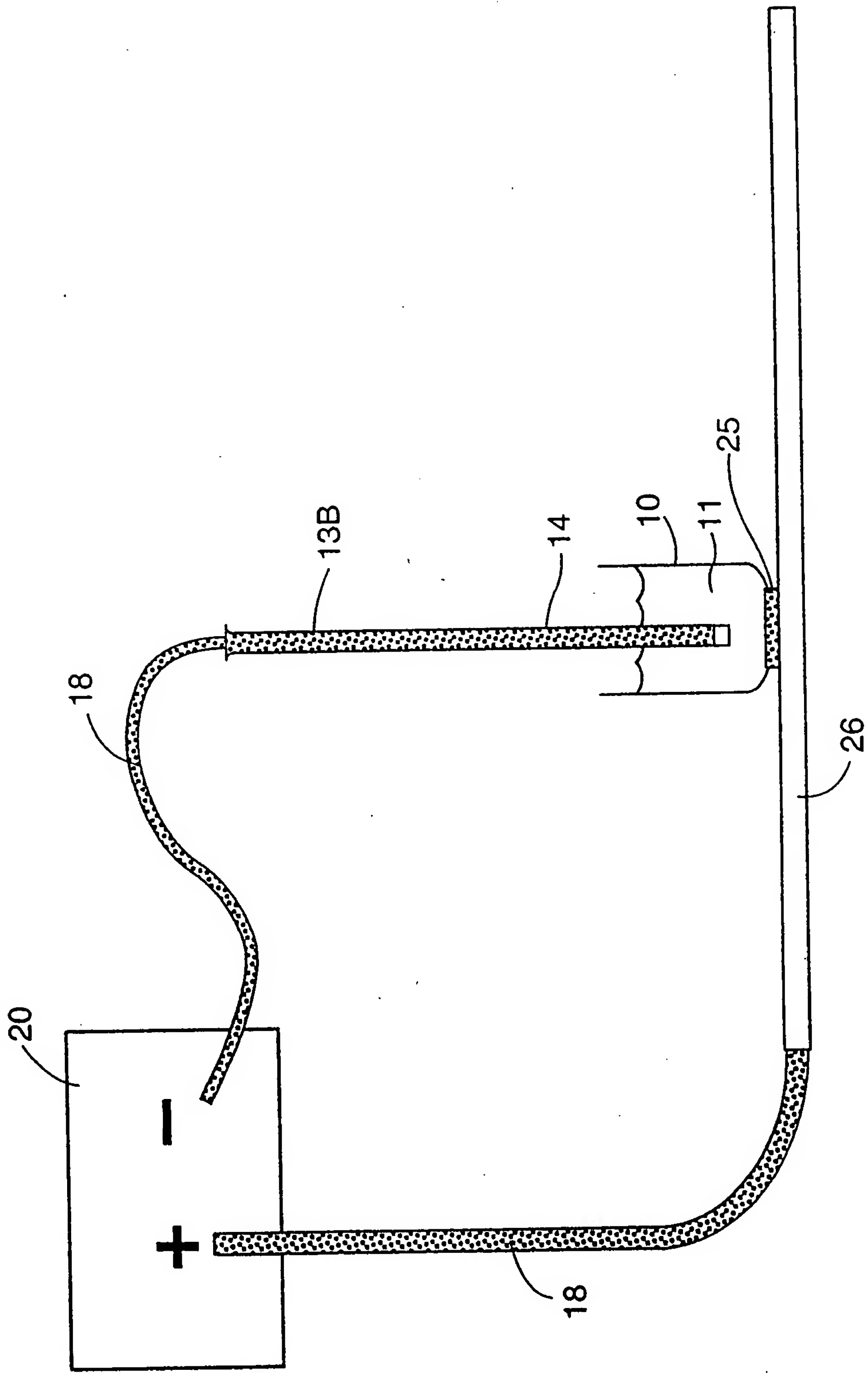


FIG. 52

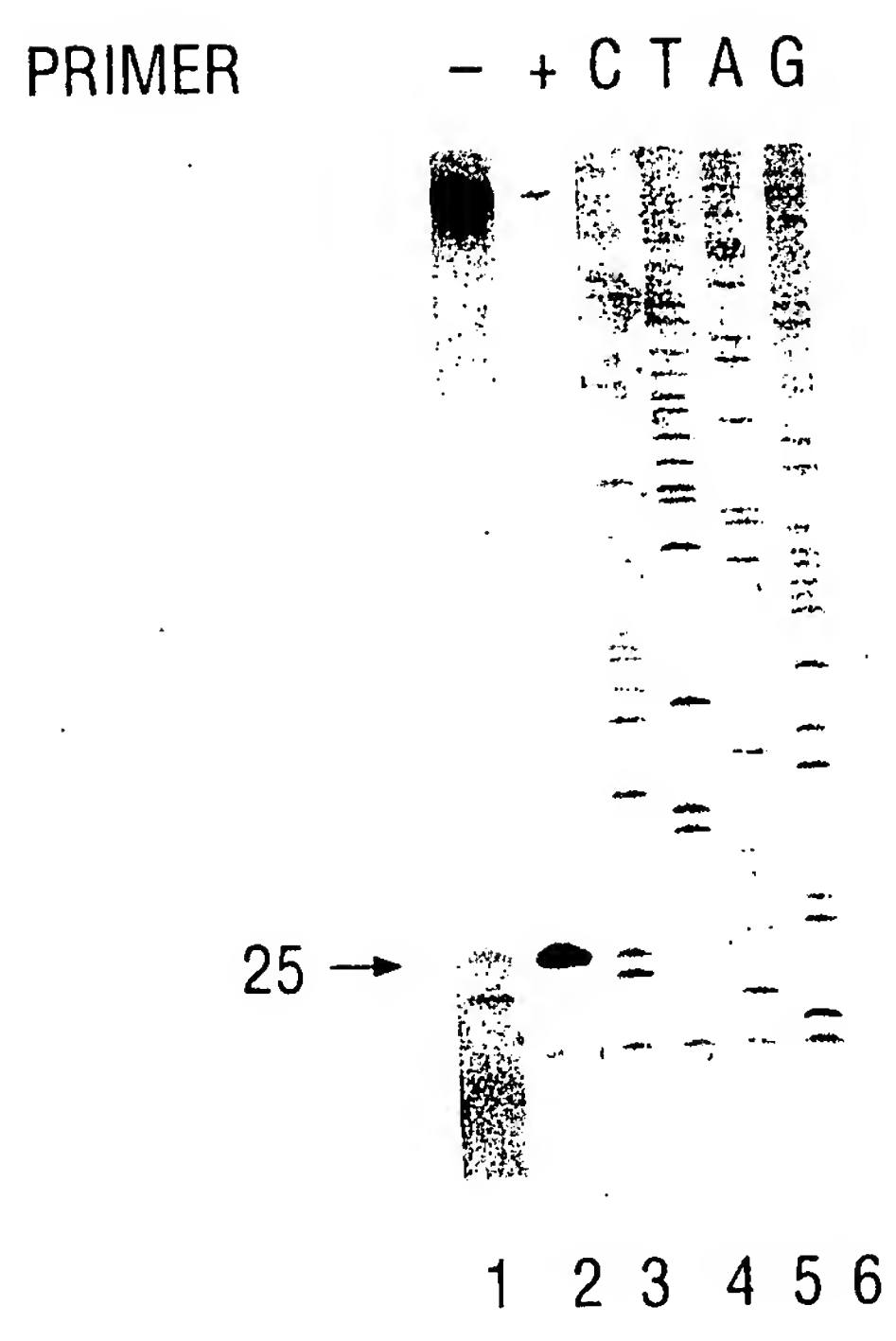
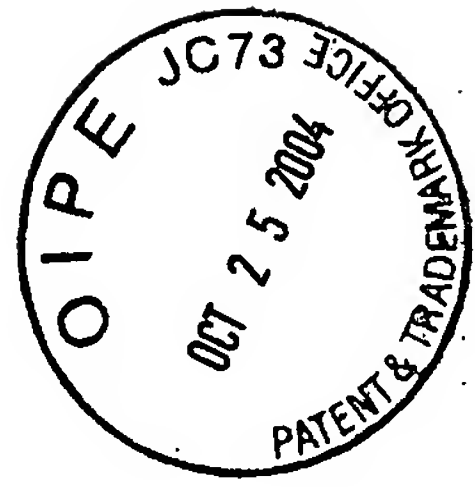


FIG. 53

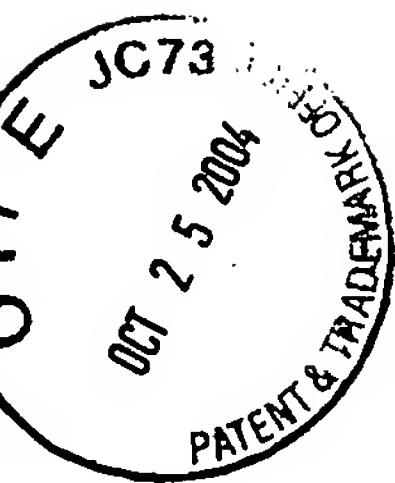


FIG. 54A



FIG. 54B



FIG. 54C



FIG. 54D

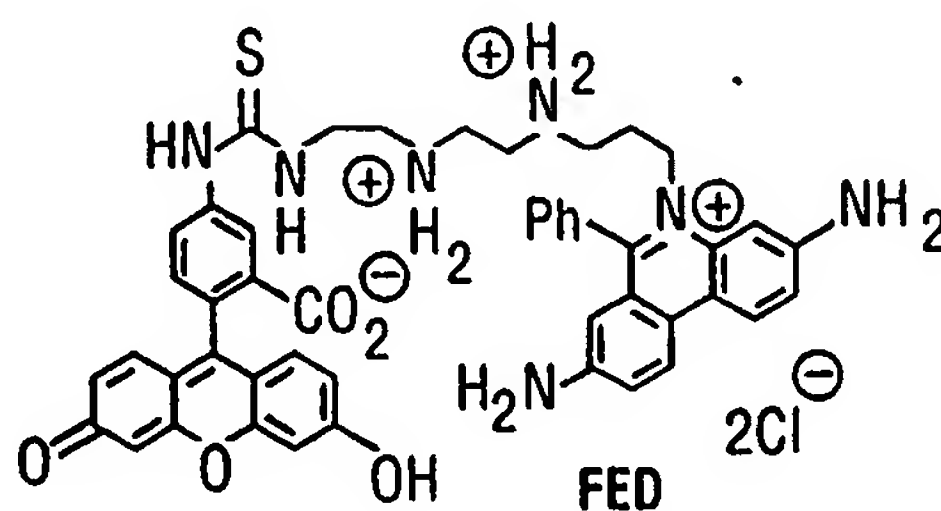
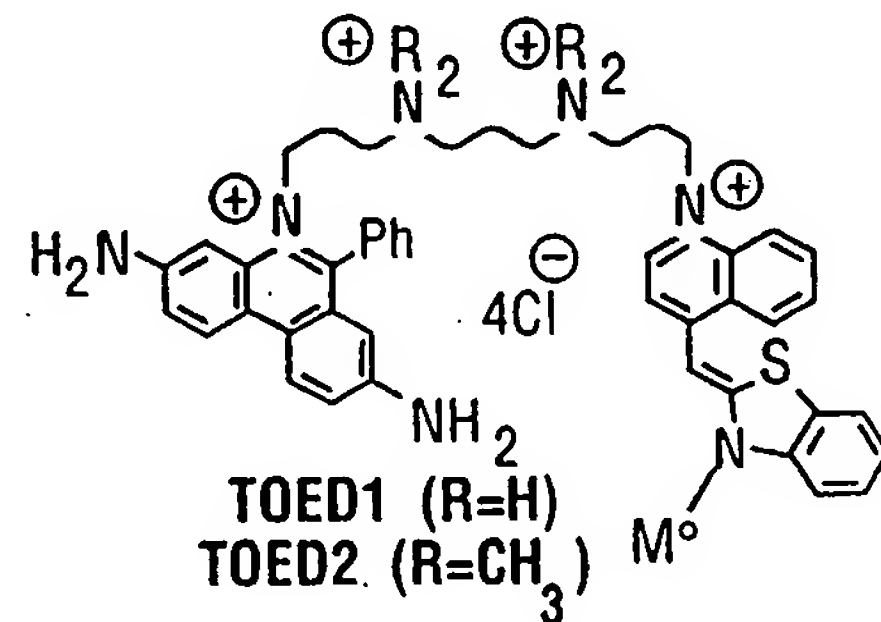
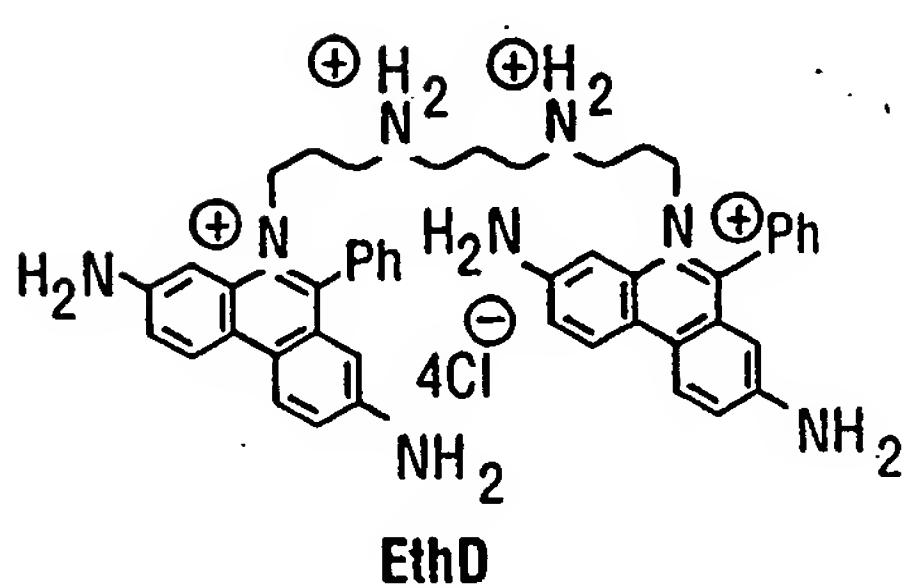
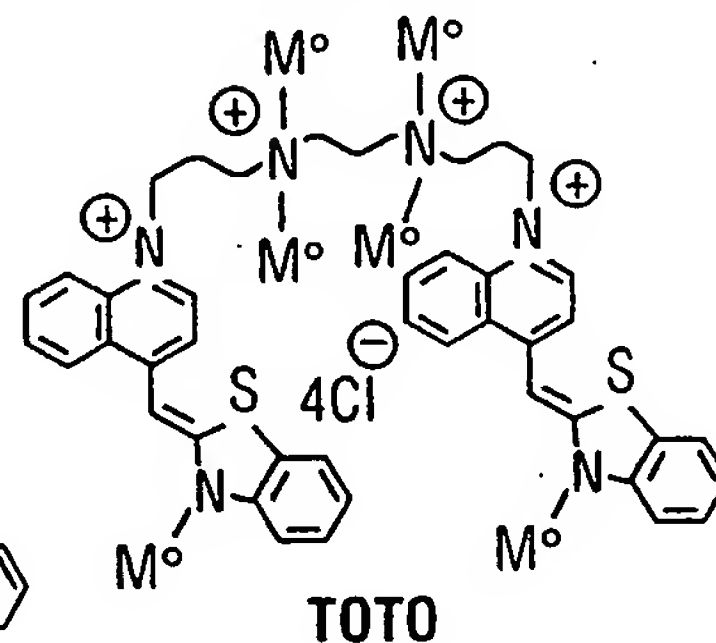
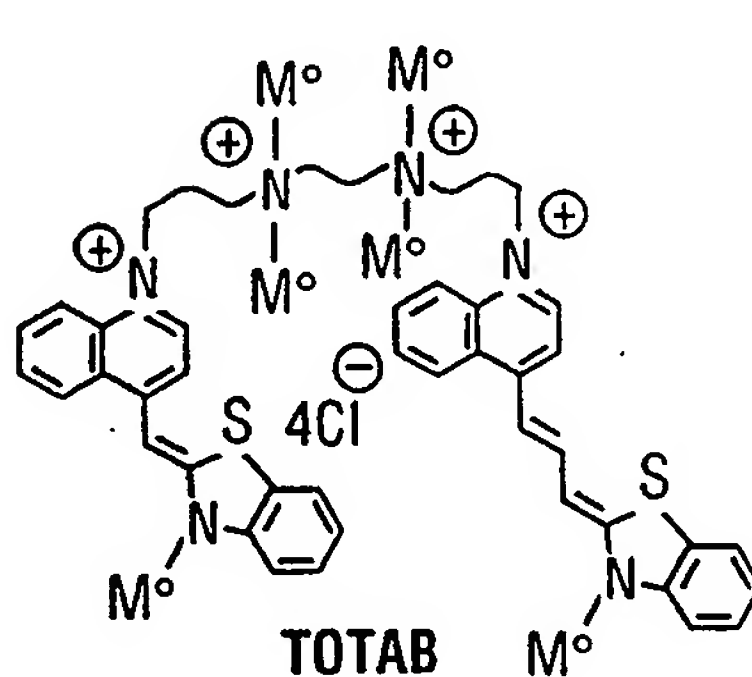
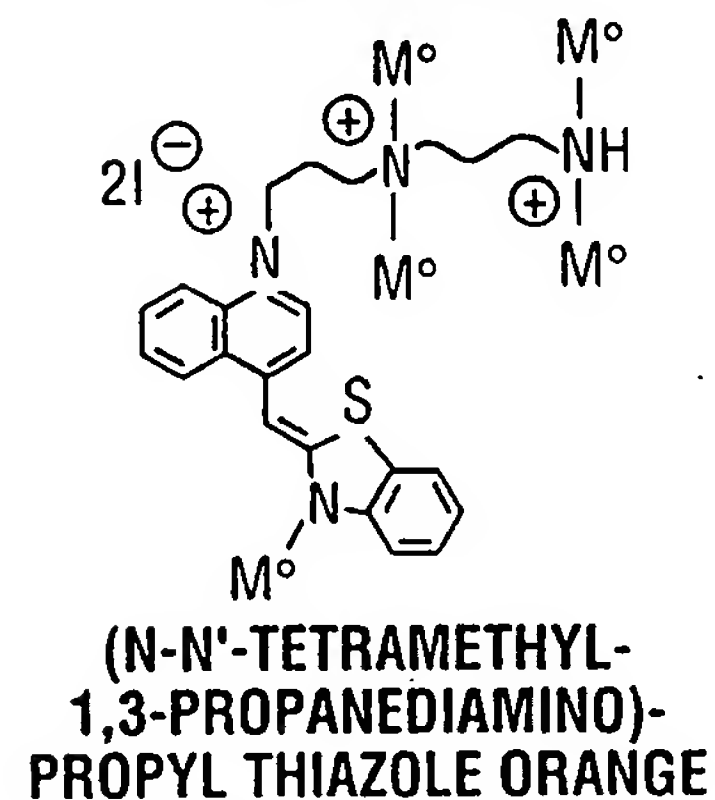
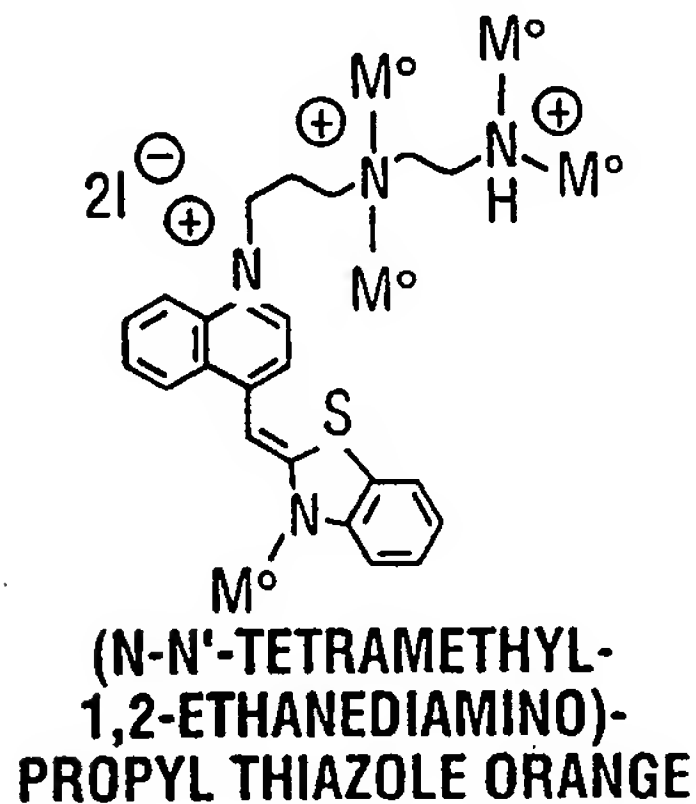
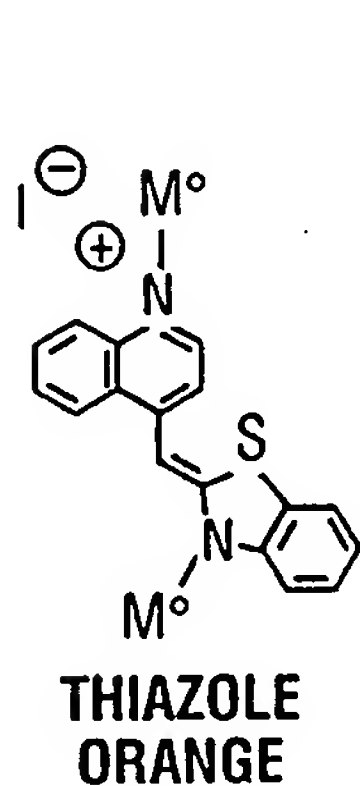
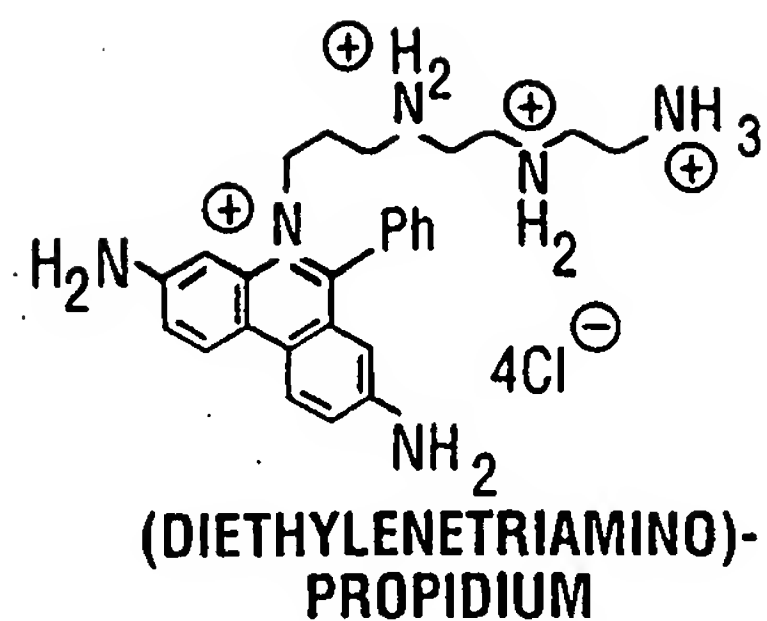
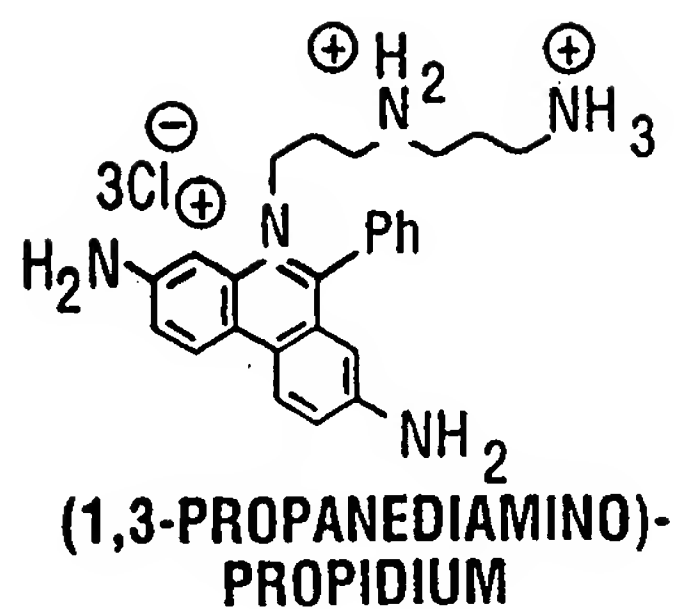
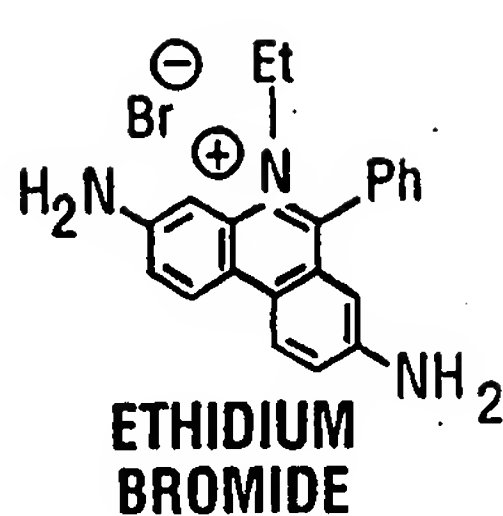
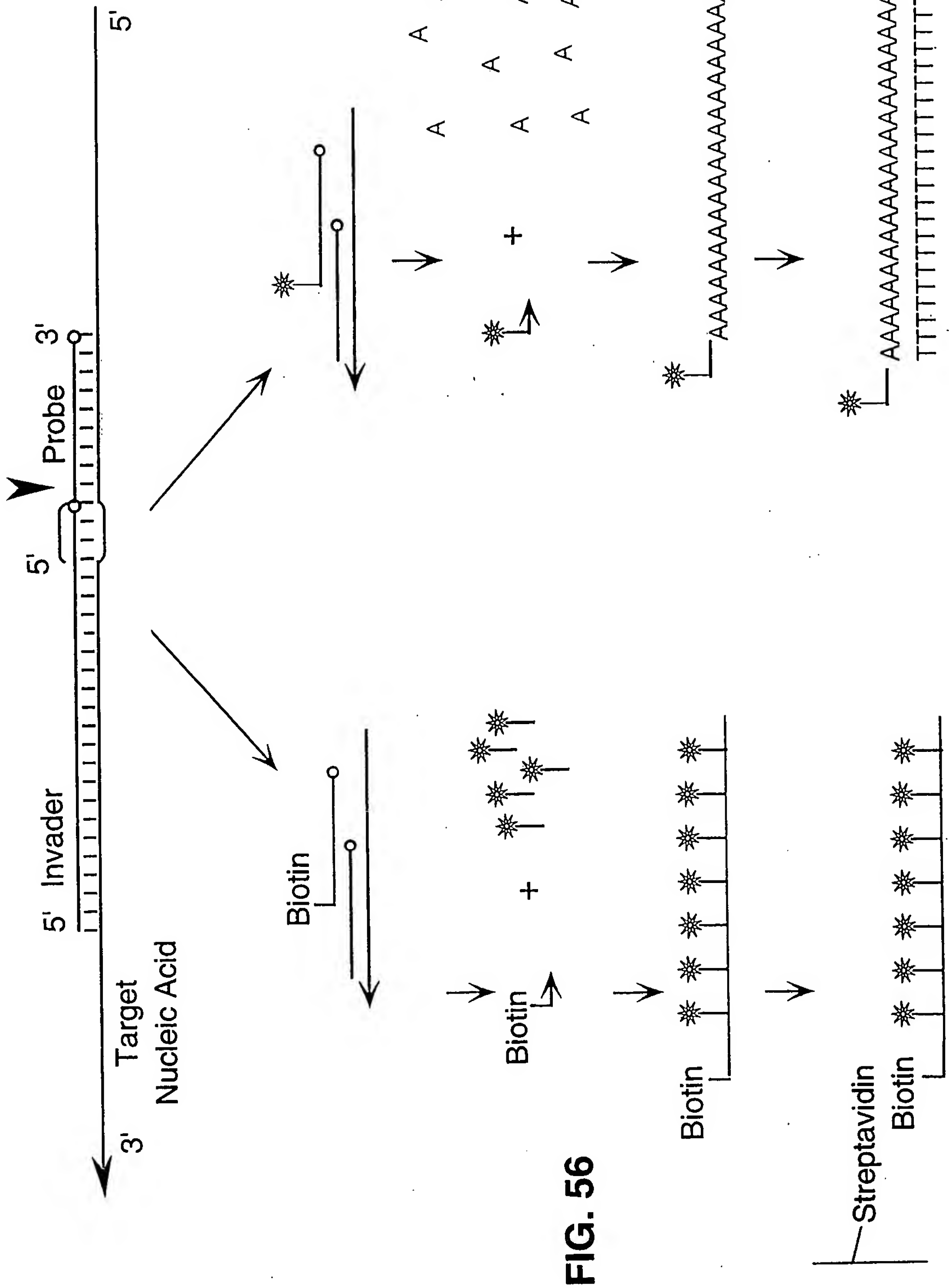


FIG. 55



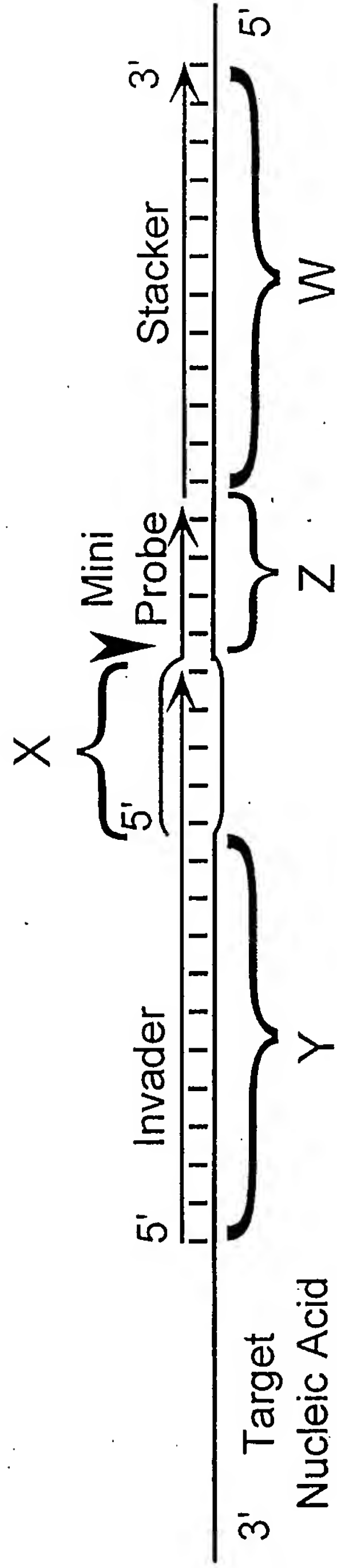
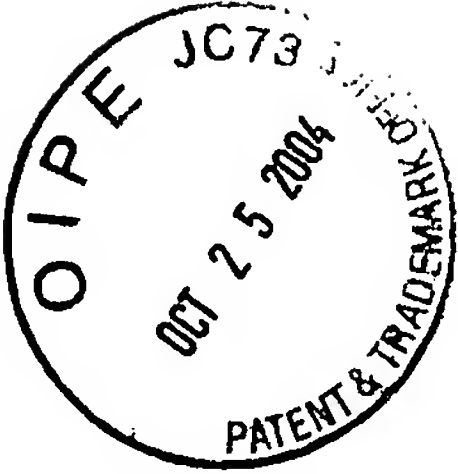


FIG. 57

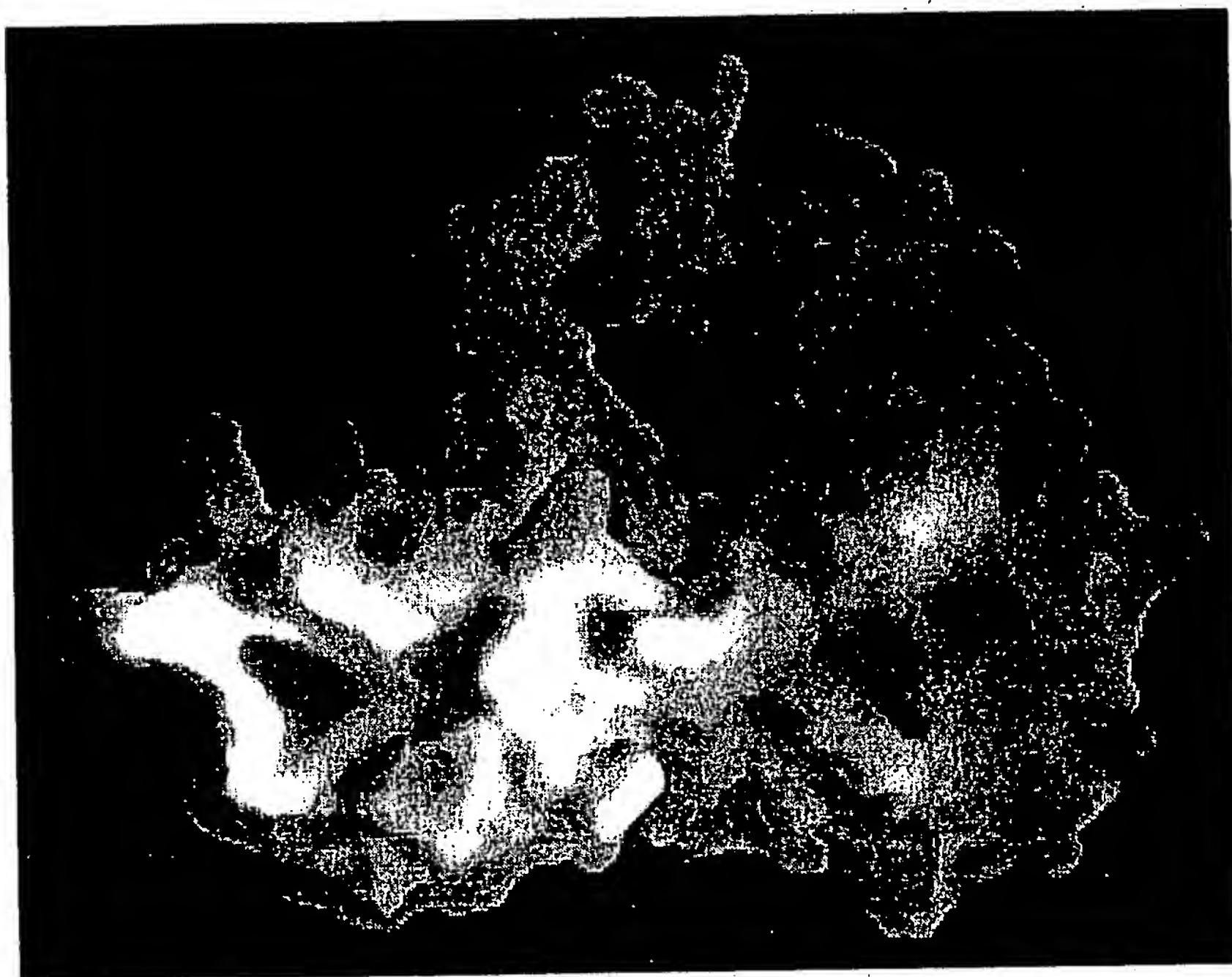
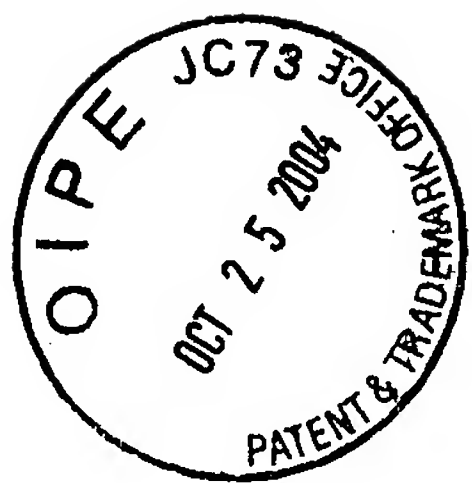
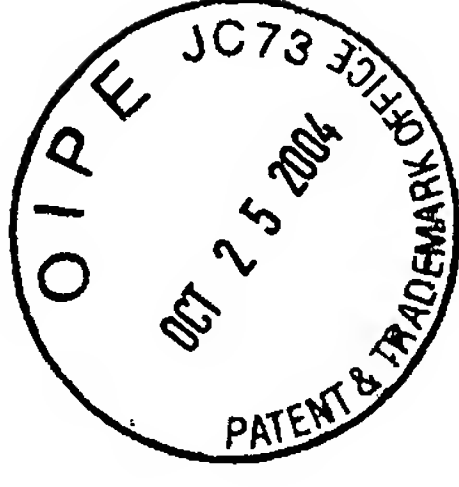


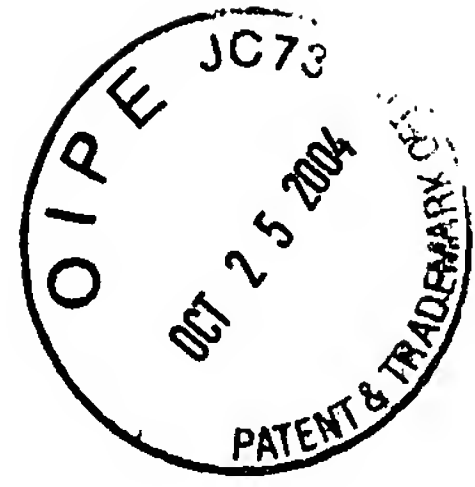
FIG. 58



| | 10 | 20 | 30 | 40 | 50 | 60 | 70 | | | | | |
|---|-----------|------------|----------|-----------|----------|--------|----------|-----------|------------|--------------|--------------|---------------|
| 1 | MGVQ----- | FGDFIPK-- | NIISFEDL | KGKKVAID | GMNALYQF | LT | SIRLRDGS | PLNRKGEIT | SAYNGVFY | MJAFEN1. PRO | | |
| 1 | MGVP----- | IGEIIIPR-- | KEIELENL | YGKKIAID | ALNAIYQF | LS | TIRQKDG | TPLMDSKGR | ITSHLSGLFY | PFUFEN1. PRO | | |
| 1 | MGIQGLAKL | IADVAPSA | IRENDIKS | YFGRKVAID | ASMSIYQF | LI | AVRQ-GGD | VLQNEEG | ETTS | SHLMGMFY | HUMFEN1. PRO | |
| 1 | MGIHGLAKL | IADVAPSA | IRENDIKS | YFGRKVAID | ASMSIYQF | LI | AVRQ-GGD | VLQNEEG | ETTS | -LMGMFY | MUSFEN1. PRO | |
| 1 | MGIKGLNAI | ISEHVPSA | IRKSDIKS | FFGRKVAID | ASMSLYQF | LI | AVRQQDGG | QLTNEAG | ETTS | SHLMGMFY | YST510. PRO | |
| 1 | MGVHSFWDI | AG---- | PTARPVRL | ESLEDKR | MAVDASI | WIYQF | LKAVRDQ | EGNAVK | N----- | SHITGFFR | YSTRAD2. PRO | |
| 1 | MGVSGLWNI | LE---- | PVKRPVKL | ETLVNKR | LAI | DA | SIWIYQF | LKAVRDQ | EGNQ | LKS----- | SHVVGFFR | SPORAD13. PRO |
| 1 | MGVQGLWKL | LE---- | CSGROVSP | EALEGKIL | AVDISI | WLNQAL | KGVDRH | GN | SIEN----- | PHLLTLFH | HUMXPG. PRO | |
| 1 | MGVQGLWKL | LE---- | CSGHRVSP | EALEGKVL | AVDISI | WLNQAL | KGVDRS | HGN | VIEN----- | AHLLTLFH | MUSXPG. PRO | |
| 1 | MGVQGLWKL | LE---- | CSGRPINP | GTLEGKIL | AVDISI | WLNQAV | KGARDR | QGN | AIQN----- | AHLLTLFH | XENXPG. PRO | |
| 1 | MTINGIWE | WANHVV-- | --RKVP | NETMRD | KTLSID | GHIWL | YESLKG | CEAHHQ | QT----- | PNSYLVT | FTT | CELRAD2. PRO |

| | 80 | 90 | 100 | 110 | 120 | 130 | 140 | | | | | | | | | | | |
|----|--------|--------|----------|---------|--------|---------|---------|--------|---------|--------|--------|--------|--------------|--------------|-------|--------------|---------------|--------------|
| 64 | KTIHL | LENDIT | PIWVFD | GEPPKL | KEKTR | KVRRE | MKEKAEL | KMKEAI | KK---- | EDFEEA | AKYAKR | VSYLTP | MJAFEN1. PRO | | | | | |
| 64 | RTINL | MEAGIK | PVYVFD | GEPP | EFKKKE | LEKRR | REAREE | AEK | WREALE | K----- | GEIEE | ARKYAQ | RATRVNE | PFUFEN1. PRO | | | | |
| 70 | RTIRM | MENGI | KPVYVFD | GKPPQL | KSGEL | AKRSERR | AEAEK | QLQQA | AA---- | GAE | OEVEK | FTKRLV | KVTK | HUMFEN1. PRO | | | | |
| 69 | RTIRM | -ENG | IKPVYVFD | GKPPQL | KSGEL | AKRSERR | AEAEK | QLQQA | EA---- | GME | EEVEK | FTKRLV | KVTK | MUSFEN1. PRO | | | | |
| 71 | RTL | RMIDN | GIKPCY | VFDGKPP | DLKSH | ELTKR | SSRRV | ET | EKKLA-- | --EA-- | --- | TTE | LKMKQ | ERRLV | KVSK | YST510. PRO | | |
| 61 | RICKLL | YF | GIRPVF | VFDGGV | PVLK | RETIR | QRKERR | QKRES | AKSTAR | KLLAL | QLQNG | SNDN | KRDS | DEV | TM | YSTRAD2. PRO | | |
| 61 | RICKLL | FF | GIKPVF | VFDGGAP | SLKR | QTIQ | KRQARR | LDRE | ENATV | TANKLL | ALQMR | HQAM | LKRD | AD | EV | TQ | SPORAD13. PRO | |
| 61 | RLCKLL | FF | RIRPIF | VFDGDAP | LLKK | QTLV | KRRQRK | DLAS | SDSR | KTTE | KLK | TFLK | RQAI | KTER | IA | AT | VTG | HUMXPG. PRO |
| 61 | RLCKLL | FF | RIRPIF | VFDGDAP | LLKK | QTLA | KRRQRK | DSAS | IDS | RKTTE | KLK | TFLK | RQAL | KTD | RIA | AS | VTG | MUSXPG. PRO |
| 61 | RLCKLL | FF | RIRPIF | VFDGEAP | LLKR | QTLA | KRRQR | TDKAS | NDAR | KTNE | KL | RTFL | KRQAI | KAE | RIA | AT | VTG | XENXPG. PRO |
| 60 | RIQRLL | ELKI | PIVVD | NI | INASS | SAHES | KDQNE | FVPR | KRRS | FGD | SPFT | NLV-- | ----- | ----- | ----- | ----- | ----- | CELRAD2. PRO |

FIG. 59A

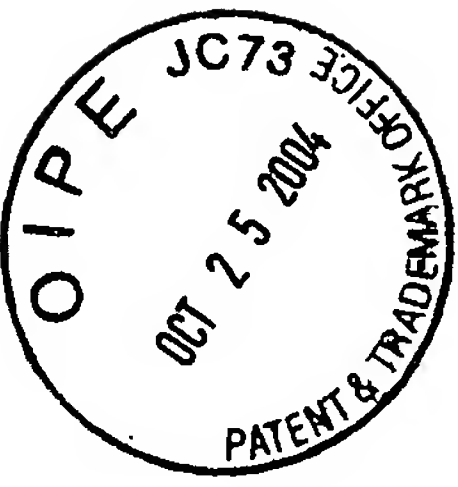


| | 150 | 160 | 170 | 180 | 190 | 200 | 210 |
|-----|--|-----|-----|-----|-----|-----|--------------|
| 130 | KMVENCKYLLSLMGIPIYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEM---- | | | | | | MJAFEN1.PRO |
| 130 | MLIEDAKKLLLELMGIPIVQAPSEGEAQAAAYMAAKGSVYASASQDYDSLFLGAPRLVRNLTITGKRKLPGK | | | | | | PFUFEN1.PRO |
| 136 | QHNDCKHLLSLMGIPLYDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ | | | | | | HUMFEN1.PRO |
| 134 | QHNDCKHLLSLMGIPLYDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHLTASEAKKLPIQ | | | | | | MUSFEN1.PRO |
| 134 | EHNEEAQKLLGLMGIPIYIIAPTAEAAQCAELAKKGKVYAAASEMDTLCYRTPFLRLHLTFSEAKKEPIH | | | | | | YST510.PRO |
| 131 | DMIKEVQELLSRFGIPIYITAPMEAAQCAELQLNLVDGIIITDDSDVFLFGGTKIYKNMFHEKNY---- | | | | | | YSTRAD2.PRO |
| 131 | VMIKECQELLRLFGLPYIYIAPOEAAEQCSKLELKLVDGIVTDDSDVFLFGGTRVYRNMFNQNKF---- | | | | | | SPORAD13.PRO |
| 131 | QMFLSQELLRLFGIPIYIAPMEAAEQCAILDITDQTSGTITDDSDIWLFGARHVYRNFFNKNKF---- | | | | | | HUMXPG.PRO |
| 131 | QMFLSQELLRLFGVPIYIAPMEAAEQCAVLDLSDQTSGTITDDSDIWLFGARHVYKNFFNKNKF---- | | | | | | MUSXPG.PRO |
| 131 | QMCLESQELLQLFGIPIYIAPMEAAEQCAILDITDQTSGTITDDSDIWLFGARHVYKNFFSQNKH---- | | | | | | XENXPG.PRO |
| 111 | DHVYKTNALLTELGIKVIIPAGDGEAQCARLEQLGVTSGCITTDYFDYFLFGGKNLYRFDFTAGT----- | | | | | | CELRAD2.PRO |
| | 220 | 230 | 240 | 250 | 260 | 270 | 280 |
| 195 | -----PELIELNEVLEDLRISLDDLDIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV | | | | | | MJAFEN1.PRO |
| 200 | NVYVE-IKPELIIILEEVVKELKLTREKLIELAILVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF | | | | | | PFUFEN1.PRO |
| 206 | EFHLSRIQLQELGLNQEQFVDLCIILGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLDPN-----KY | | | | | | HUMFEN1.PRO |
| 204 | EFHLSRVLQELGLNQEQFVDLCIILGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLDPS-----KY | | | | | | MUSFEN1.PRO |
| 204 | EIDTELVRGLDLTIEQFVDLCIMLGCDYCESIRGVGPVTALKIKT--HGSIEKIVEFIESGESNNTKW | | | | | | YST510.PRO |
| 198 | FYDAESILKLLGLDRKNMIELAQLLGSDYTNGLKGMGPVSSIEVIAEF--GNLKNFKDWYNNNGOFDKRK | | | | | | YSTRAD2.PRO |
| 198 | LYLMDDMKREFNVNQMDLIKLAHLLGSDYTMGLSRVGPVLALEILHEFPDGTGLFEFKKWFQRLSTGHAS | | | | | | SPORAD13.PRO |
| 198 | YYQYVDFHNQLGLDRNKLINLAYLLGSDYTEGIP TVGCVTAMEILNEFPBGHGLEPLKFSEWWHEAQKNP | | | | | | HUMXPG.PRO |
| 119 | YYQYVDFYSQLGLDRNKLINLAYLLGSDYTEGIP TVGCVTAMEILNEFPBGHGLEPLKFSEWWHEAQNNK | | | | | | MUSXPG.PRO |
| 198 | YYQYADIHNOGLDRSKLINLAYLLGSDYTEGIP TVGYVSAMEILNEFPGQGLEPLVKFEWWSEAQKDK | | | | | | XENXPG.PRO |
| 175 | -----SSTACLDIMHLSLGRMFM----- | | | | | | CELRAD2.PRO |

FIG. 59B

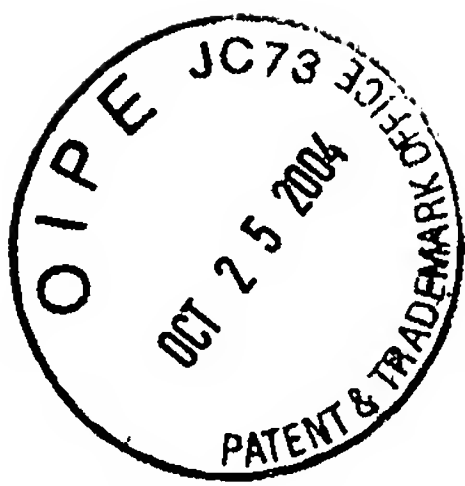
| | 290 | 300 | 310 | 320 | 330 | 340 | 350 |
|-----|--|--|------------------------------|-----|---------------|-----|---------------|
| 251 | LKKEVEYYDEIKRIFKEPKV----- | TD-- | NYSLSLKLDPDKEGIIKFLVDENDFN | YD | MJAFEN1. PRO | | |
| 265 | QKQSDVDLYAIKEFFLNPPV----- | TD-- | NYNLVWRDPDEEGILKFLCDEHDFSEE | | PFUFEN1. PRO | | |
| 269 | PVPENWLHKEAHQLFLEPEV----- | LDPE | SVELKWSEPNNEEELIKFMCGEKQFSEE | | HUMFEN1. PRO | | |
| 267 | PVPENWLHKEAQQLFLEPEV----- | VDPE | SVELKWSEPNNEEELVKFMCGEKQFSEE | | MUSFEN1. PRO | | |
| 272 | KIPEDWPYKQARMLFLDPEV----- | IDGNE | INLKWSPPKKEKELIEYLCDDKKFSEE | | YST510. PRO | | |
| 265 | QETENKFEKDLRKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVDPDLM | RSFM | KTQLGWPHE | | YSTRAD2. PRO | | |
| 268 | KNDVNTPVKKRINKLVGK--IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGIPDLDEL | RQFL | MATVGWSKQ | | SPORAD13. PRO | | |
| 268 | KIRPNPHDTKVKKKL--RTLQLTPGFPPNPAVAEAYLKPVVDDSKGSFLWGKPDLDK | IREFC | QRYFGWNRT | | HUMXPG. PRO | | |
| 268 | KVAENPYDTKVKKKL--RKLQLTPGFPPNPAVADAYLRPVVDDSRGSFLWGKPDVDK | IREFC | ORYFGWNRM | | MUSXPG. PRO | | |
| 268 | KMRPNPNDTKVKKKL--RLLDLQQSFPPNPAVASAYLKPVVDES | SKSAF | SWG RPDLEQIREFCESRFGWYRL | | XENXPG. PRO | | |
| 194 | -----EKKVSRPHL ISTAILLGCDYFORGVQNI | GIVSVFD- | ILGEFGDDGNEEIDPHVILDRFASV | RE | CELRAD2. PRO | | |
| | 360 | 370 | 380 | 390 | 400 | 410 | 420 |
| 300 | RVKKHVDKLYNLIA----- | | | | | | MJAFEN1. PRO |
| 314 | RVKNGLERLKKAI----- | | | | | | PFUFEN1. PRO |
| 320 | RIRSGVKRLSKSRQGS-TQGRLD DFFKVT-- | | | | | | HUMFEN1. PRO |
| 318 | RIRSGVKRLSKSRQGS-TQGRLD DFFKVT-- | | | | | | MUSFEN1. PRO |
| 323 | RVKSGISRLKKGLKSG-IQGRLDGFFOVV-- | | | | | | YST510. PRO |
| 335 | KSDEIL IPIIRDVNKRKK----- | | | | | | YSTRAD2. PRO |
| 337 | RTNEVLLPVIQDMHKKOF----- | | | | | | SPORAD13. PRO |
| 336 | KTDES LFPVLKQLDAQQTQLRIDSF | FRLAQQEKEDAKRIKSQRLNRAVTCMLRKEKEAA | SEIEAVSVAM | | | | HUMXPG. PRO |
| 336 | KTDES LYPVLKHLNAHQ TQLRIDSF | FRLAQQEKQDAKLKSHRLSRAVTCMLRKEEKAPELTKVTEAM | | | | | MUSXPG. PRO |
| 336 | KTDEVLLPVLKQLNAQQ TQLRIDSF | FRLEQHEAAG--LKSQRLRRAVTCMKRKERDVEAE | EEVAAVAM | | | | XENXPG. PRO |
| 257 | EIPARSED TQRKRLRRKKYNFPVGF | PNCD AVHNAITMYLRPPVSSEIPKIIPR---- | | | | | CELRAD2. PRO |

FIG. 59C



| | 430 | 440 | 450 | 460 | 470 | 480 | 490 |
|-----|---|-------|-------|-------|-------|-----------------------|--------------|
| 314 | ----- | ----- | ----- | ----- | ----- | ----- | MJAFEN1.PRO |
| 327 | ----- | ----- | ----- | ----- | ----- | ----- | PFUFEN1.PRO |
| 348 | ----- | ----- | ----- | ----- | ----- | -----GSL | HUMFEN1.PRO |
| 346 | ----- | ----- | ----- | ----- | ----- | -----GSL | MUSFEN1.PRO |
| 351 | ----- | ----- | ----- | ----- | ----- | -----PK-T | YST510.PRO |
| 357 | KRINEFF | ----- | ----- | ----- | ----- | ----- | YSTRAD2.PRO |
| 359 | SNLTQFFEGGNTNVYAPRVAYHFKSKRLENALSSFKNQISNQSPMSEEQADADAFGESKGSDELOSRI | | | | | | SPORAD13.PRO |
| 406 | EKEFELLDKAKRKTKQKRGITNTLEESSSLKRRLSDSKRNTCGGFLGETCLSESSDGSSEHAESSLM | | | | | | HUMXPG.PRO |
| 406 | EKEFELLDKAKRKTKQKRGITNTLEESSSLKRRLSDSKRNTCGGFLGETCLSESSDGSSEHAESSLM | | | | | | MUSXPG.PRO |
| 403 | ERECTNQKRGQKNTKS | ----- | ----- | ----- | ----- | ----- | XENXPG.PRO |
| 322 | MKECGWPATRTQKELALSIRRKVHLTTTVAQTRIPDFFAATKSKNFTPIVEPCE | | | | | | CELRAD2.PRO |
| | 500 | 510 | 520 | 530 | 540 | 550 | 560 |
| 314 | ----- | ----- | ----- | ----- | ----- | -----NKTQKTL | MJAFEN1.PRO |
| 327 | ----- | ----- | ----- | ----- | ----- | -----KSGKQSTL | PFUFEN1.PRO |
| 352 | SAKRKEPEPKGST | ----- | ----- | ----- | ----- | -----KKKAKTGAAG | HUMFEN1.PRO |
| 350 | SAKRKEPEPKGPA | ----- | ----- | ----- | ----- | -----KKKAKTGGAG | MUSFEN1.PRO |
| 354 | KEQLAAAKRAQE | ----- | ----- | ----- | ----- | -----NKKLNKNKNK | YST510.PRO |
| 364 | ----- | ----- | ----- | ----- | ----- | -----KK | YSTRAD2.PRO |
| 429 | RRKKMMASKNSSDSDSEDNFLASLTPKTNSSSISIENLPRKTKLSTSL | | | | | -----KKP | SPORAD13.PRO |
| 476 | NVQRRTAKEPKTSASDSONSVKEAPVKNKGATTSSSSDSDDDGGKEKMLVLTARSVFGKKRRKLRRARG | | | | | | HUMXPG.PRO |
| 469 | SARQRSAAESSKIGCSDVPDLVRDSPHGRQGCSTSSDSEDGEDKAKTVLVTARPVFGKKRRKLKSMK | | | | | | MUSXPG.PRO |
| 458 | -----GSSSDAEDLPSGLIDKQSQSGIVGROKASNKVSSSSDDEDRVTMVTAKPVFQGGKTKSKTMKE | | | | | | XENXPG.PRO |
| 387 | WMRKRKRSQPQLQHHAKRQVPDRK | ----- | ----- | ----- | ----- | -----RSVKIRAFKPYPTDVI | CELRAD2.PRO |

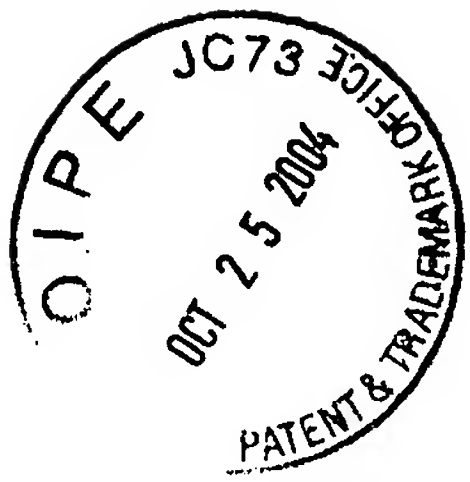
FIG. 59D



322 DAWFKZ
335 ESWFKR
375 KFKRGK
373 KFRRGK
377 VTKGRR
390 - - -RKM
483 SKRRRK
546 RKRKTZ
538 RRKKKT
523 TVKRK
429 ELGDSD

MJAFEN1 . PRO
PFUFEN1 . PRO
HUMFEN1 . PRO
MUSFEN1 . PRO
YST510 . PRO
YSTRAD2 . PRO
SPORAD13 . PRO
HUMXPG . PRO
MUSXPG . PRO
XENXPG . PRO
CELRAD2 . PRO

FIG. 59E



S-33

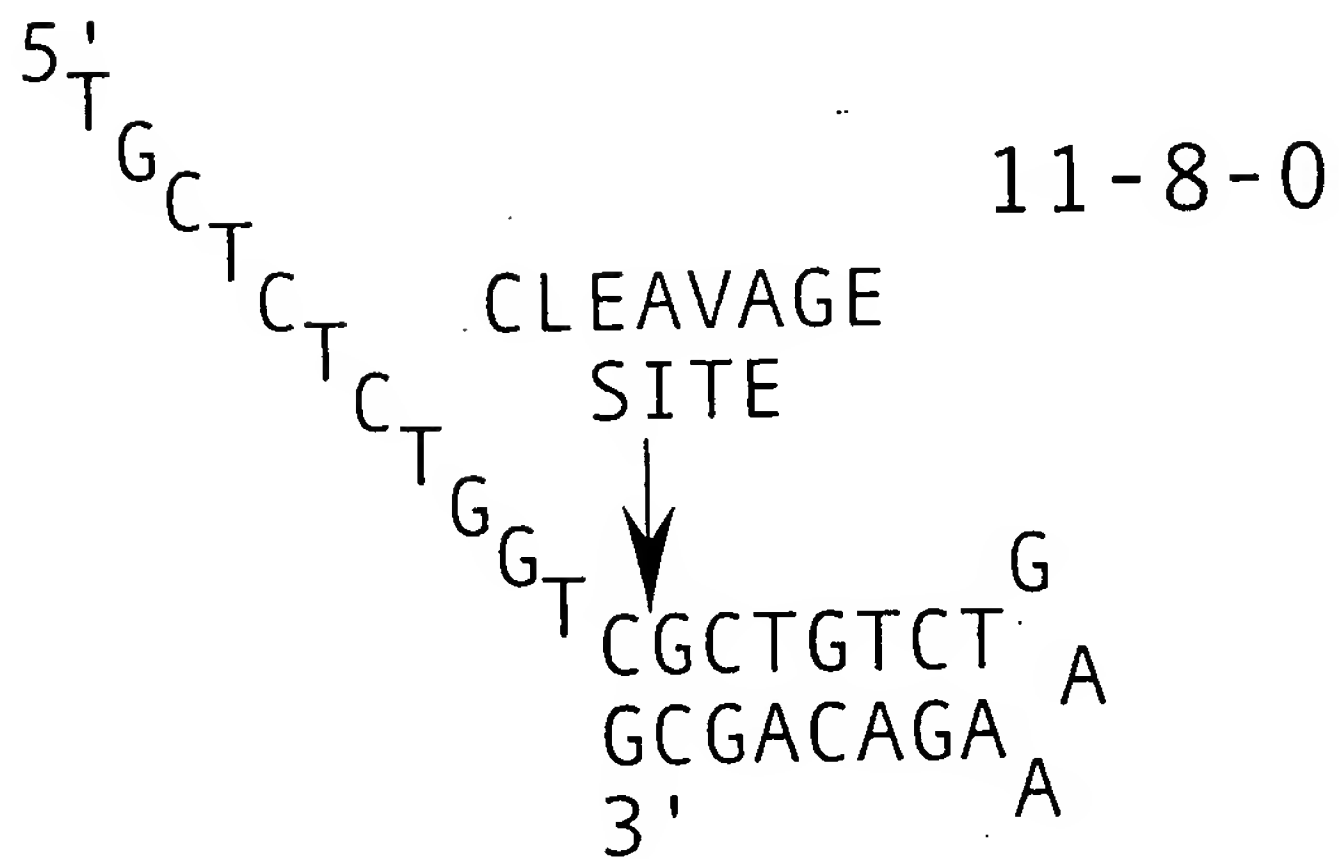
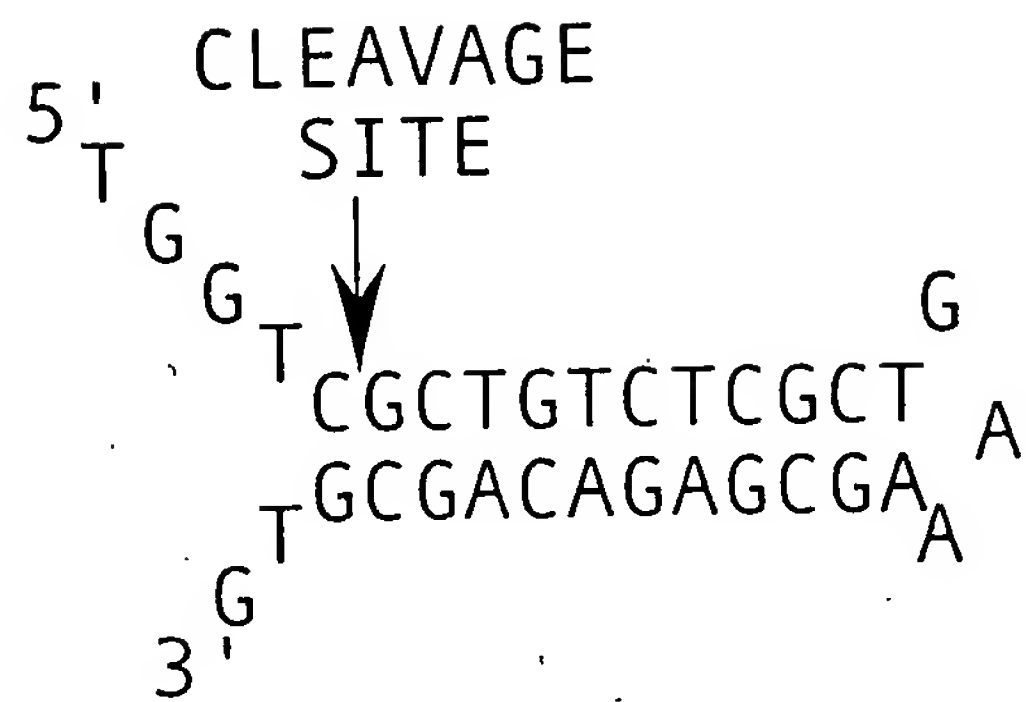
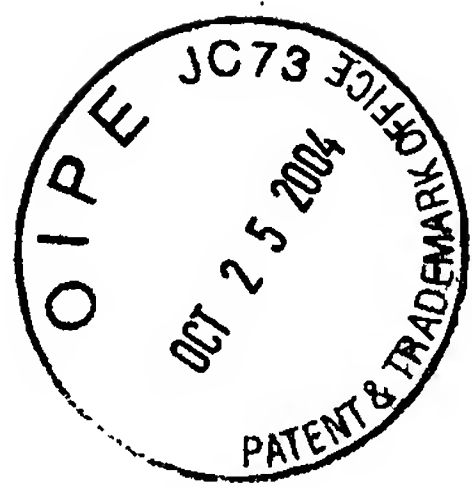
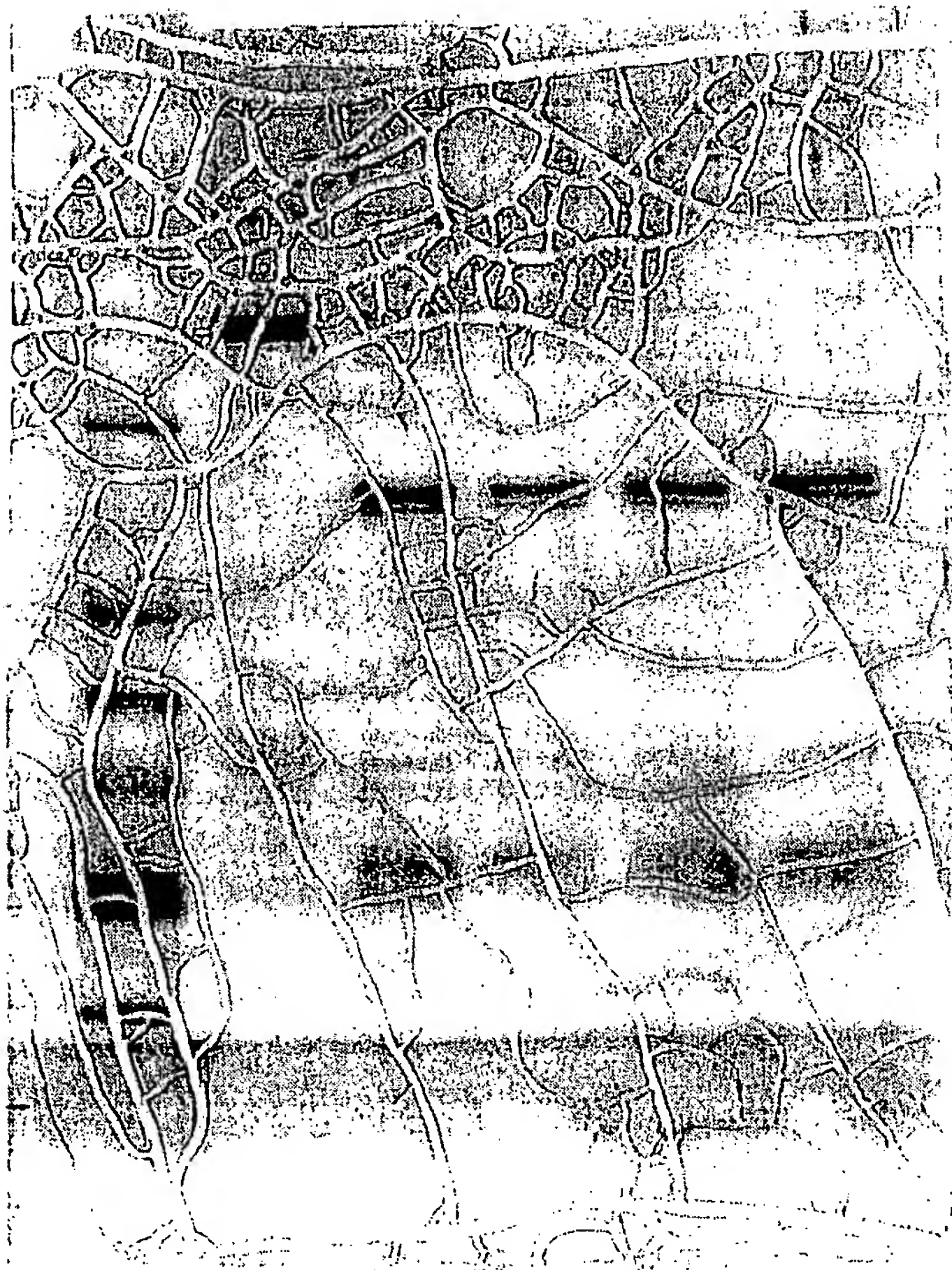


FIG. 60



1 2 3 4 5



← UNCUT

← CLEAVED

FIG. 61

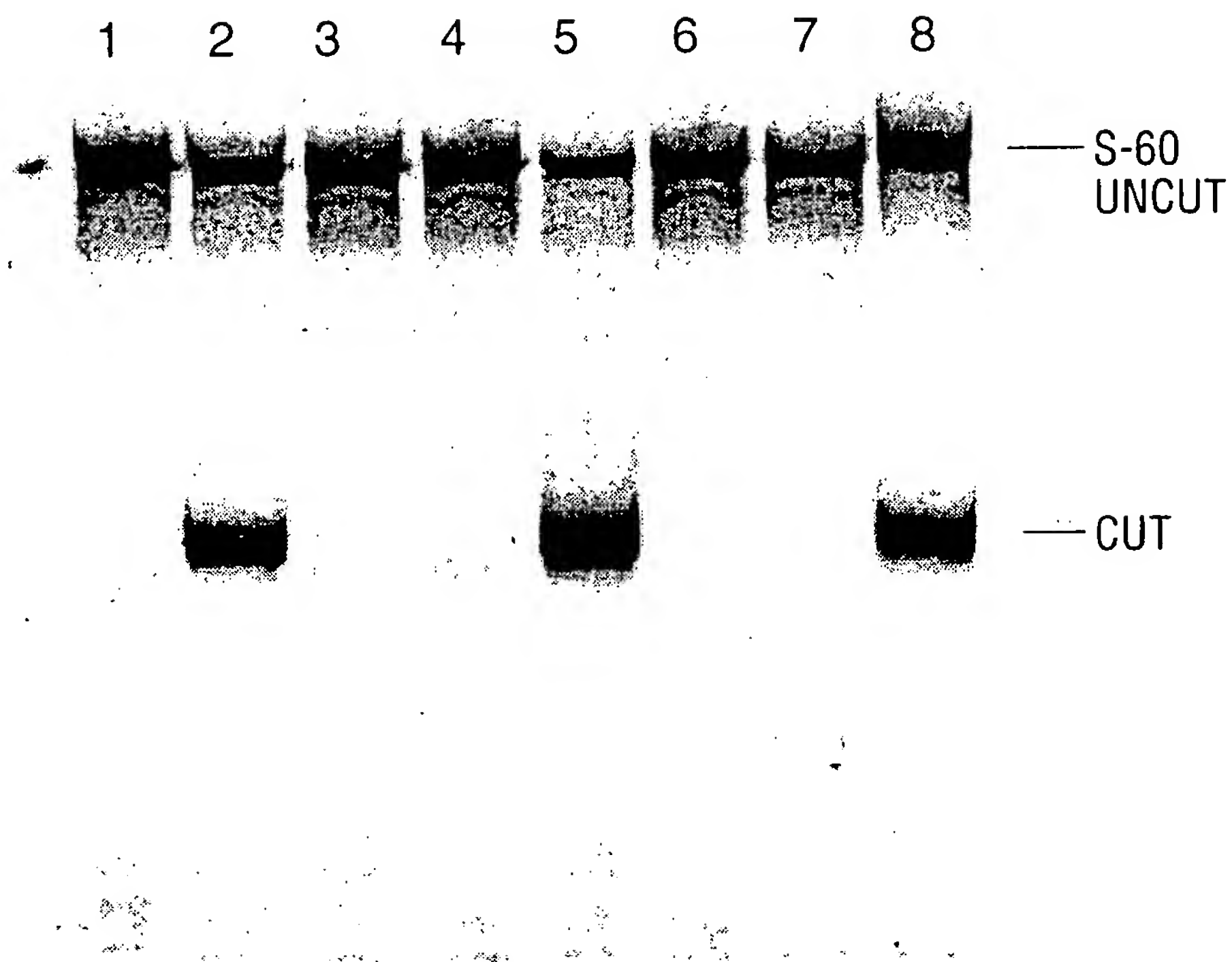
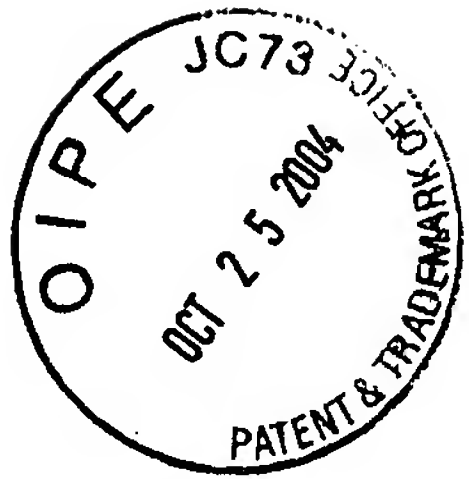


FIG. 62

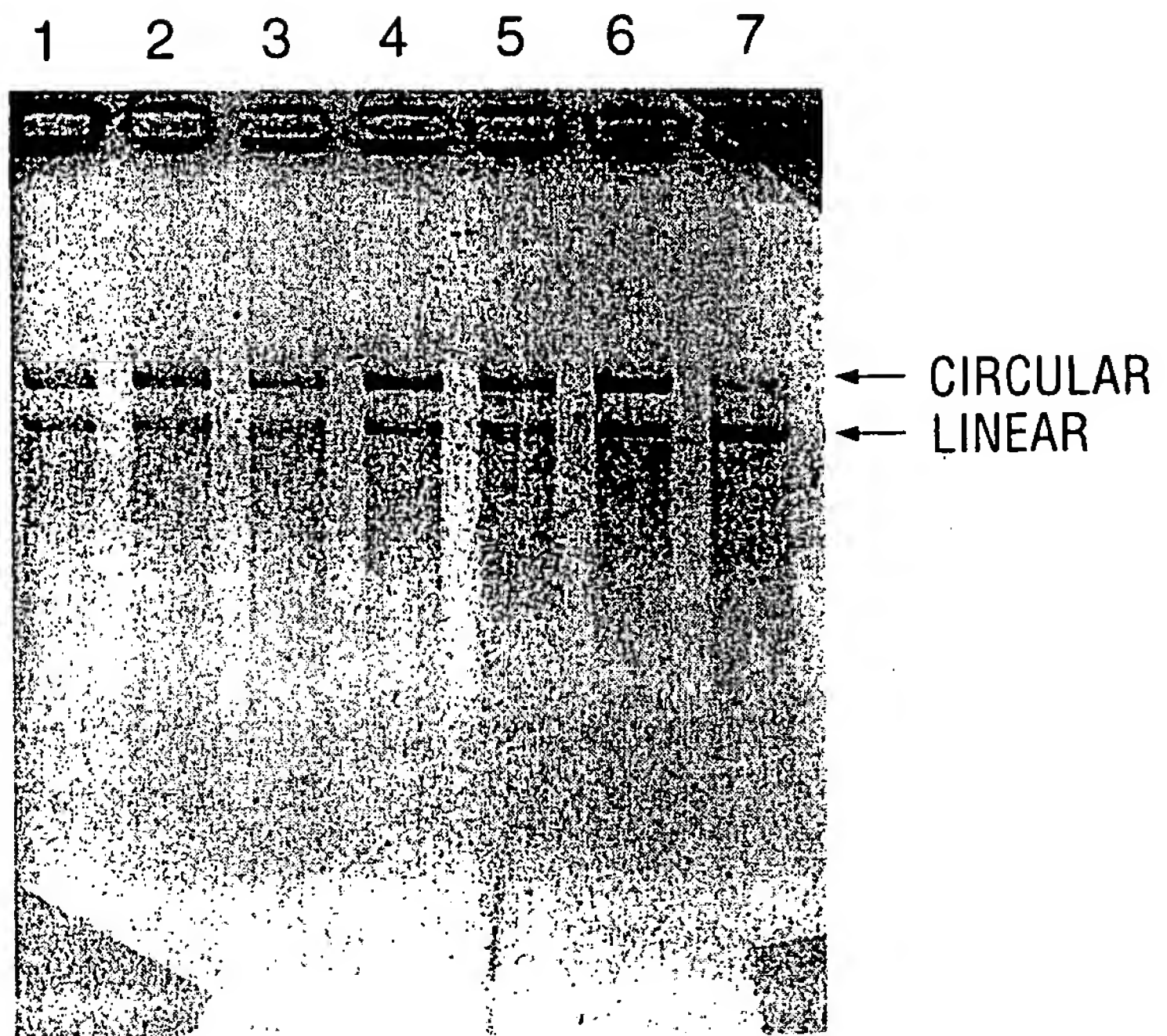
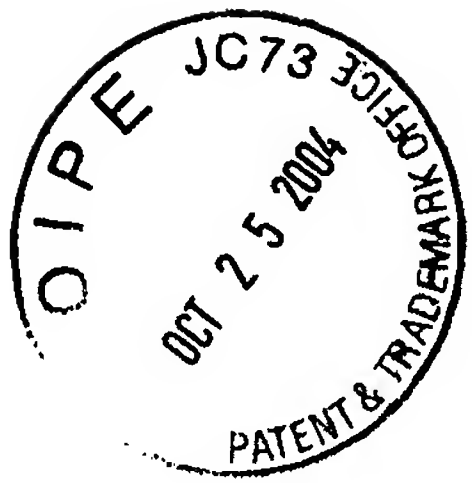


FIG. 63

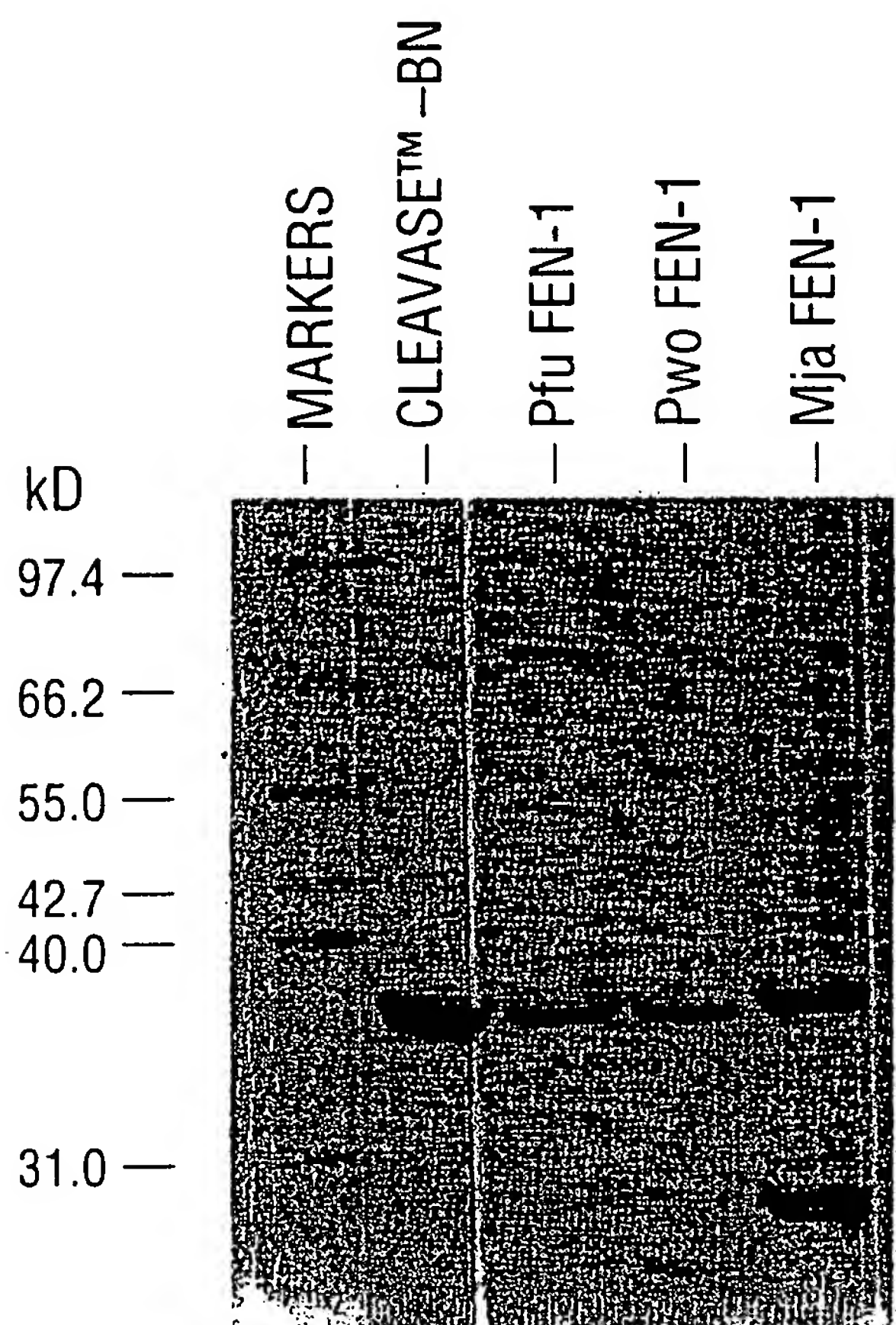


FIG. 64

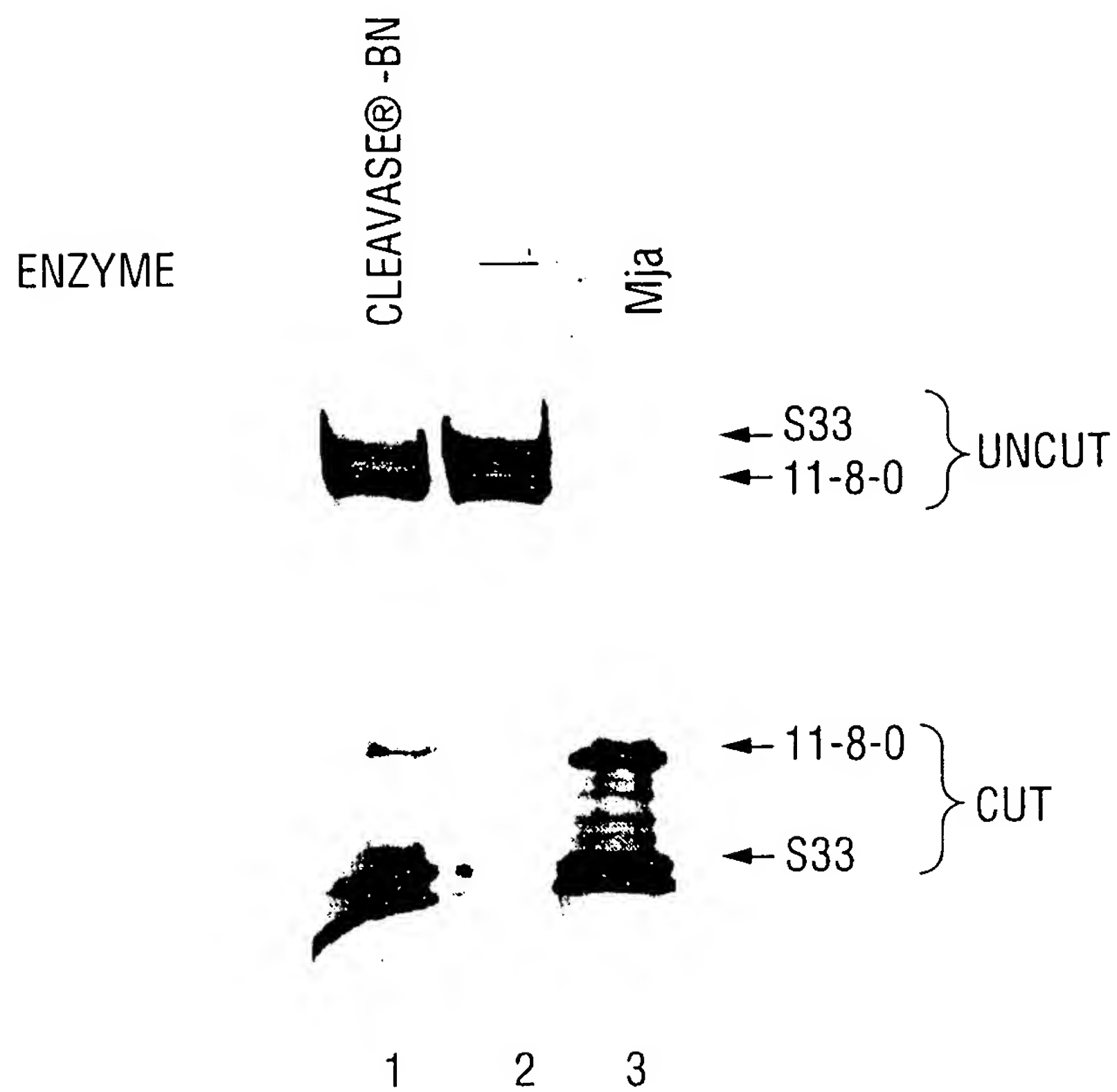
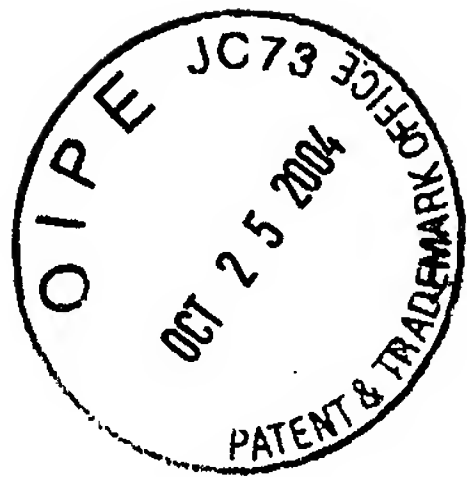
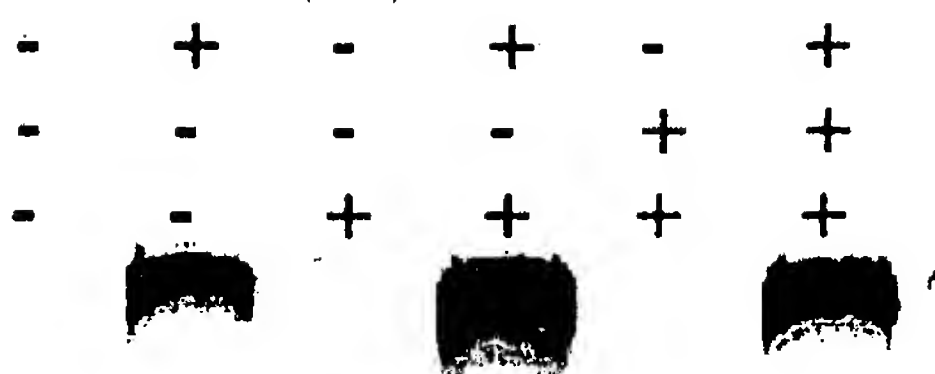
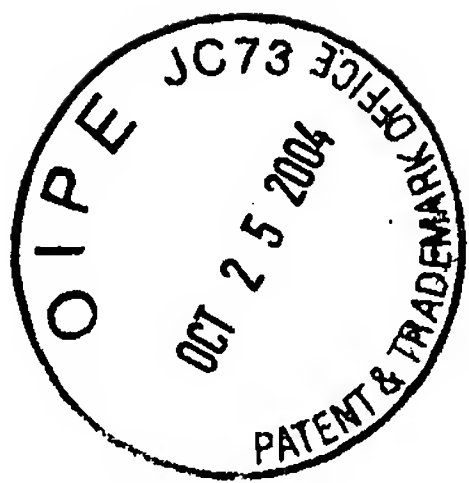
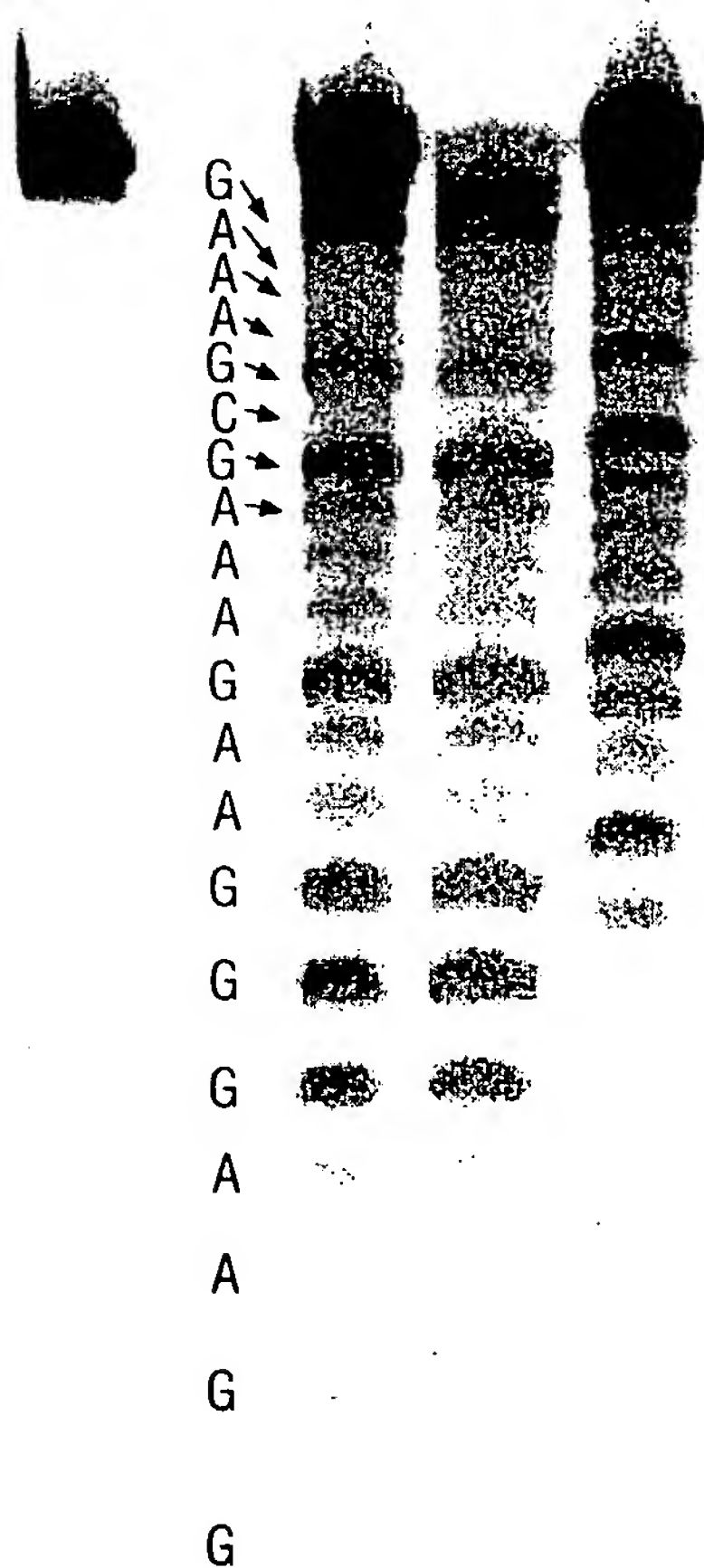


FIG. 65



TERMINAL TRANSFERASE
ALKALINE PHOSPHATASE
THERMAL DEGRADATION



5'-nAGAAAggaagggaagaaagcgaaagG-3'

FIG. 66

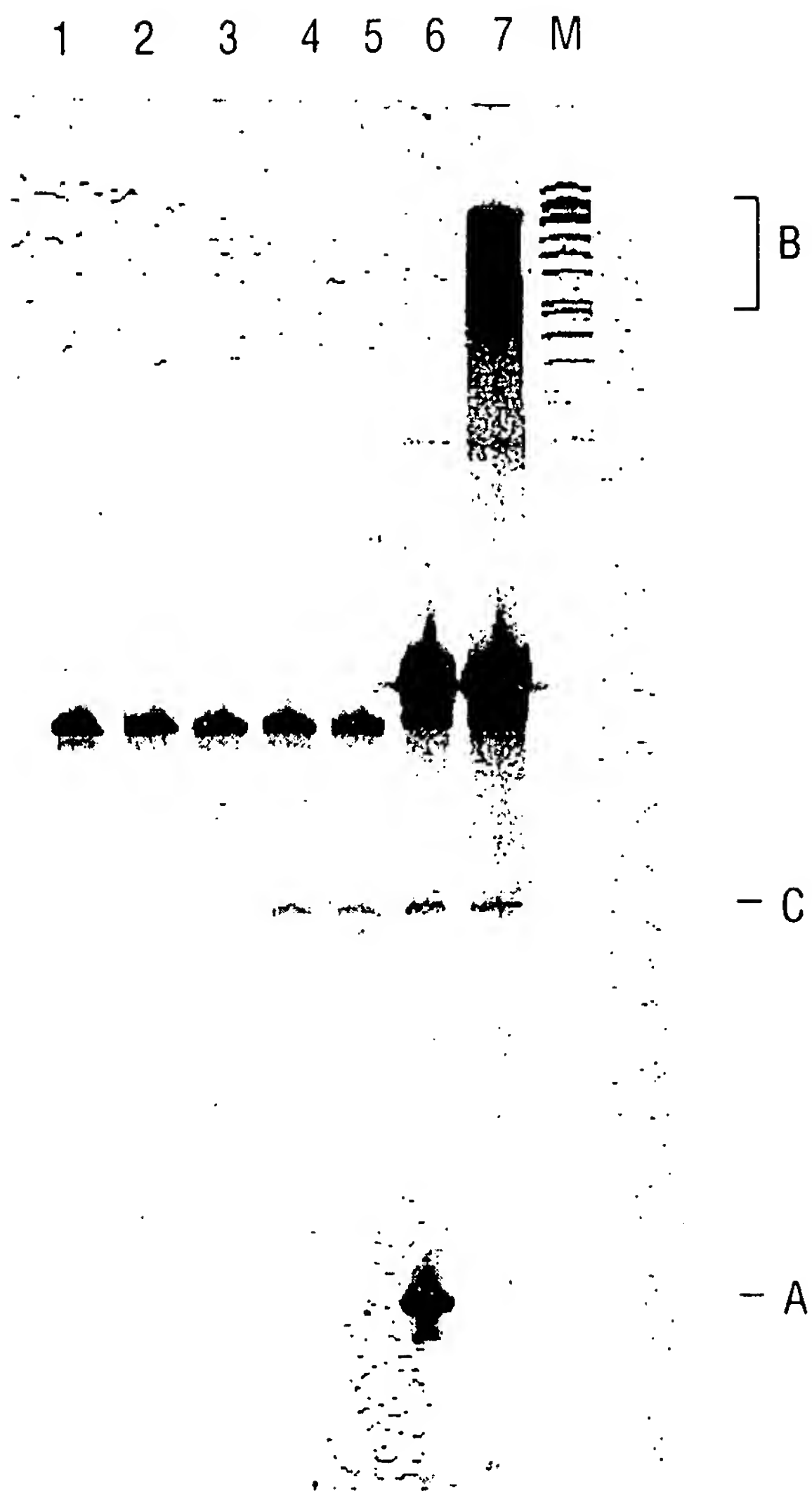
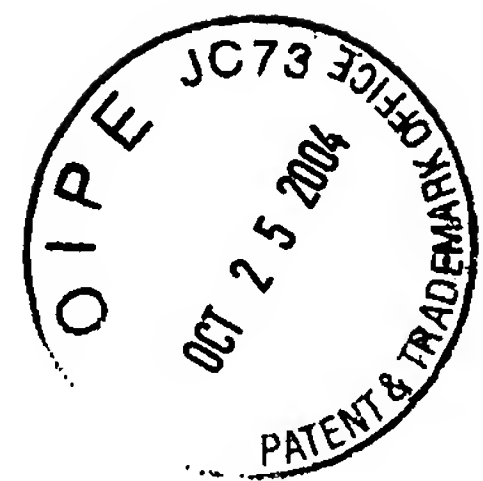


FIG. 67

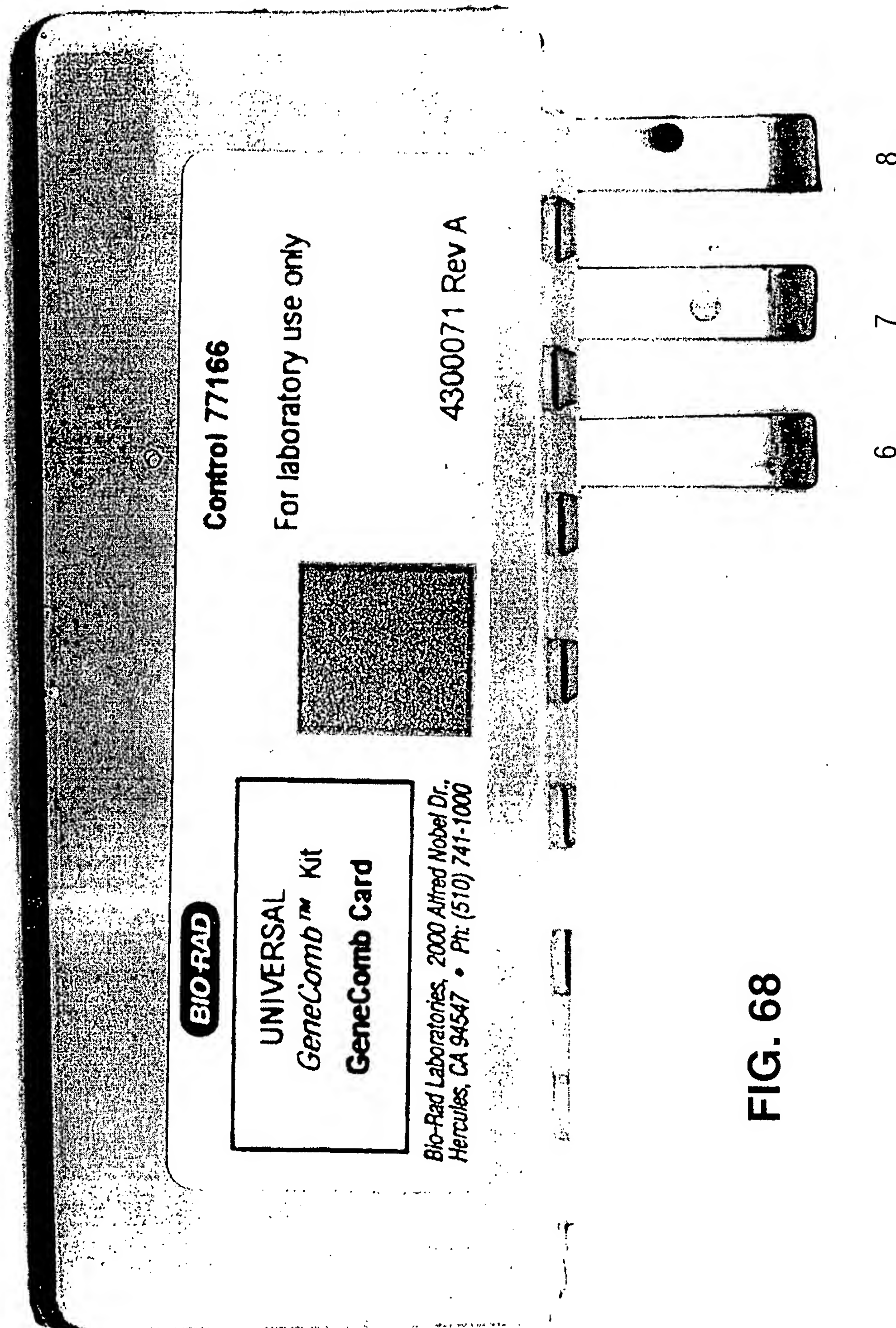
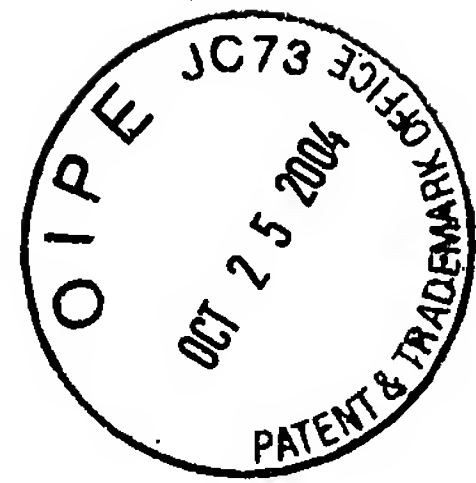


FIG. 68

O I P E J C 7 3
O C T 2 5 2 0 0 4
P A T E N T & T R A D E M A R K O F F I C E

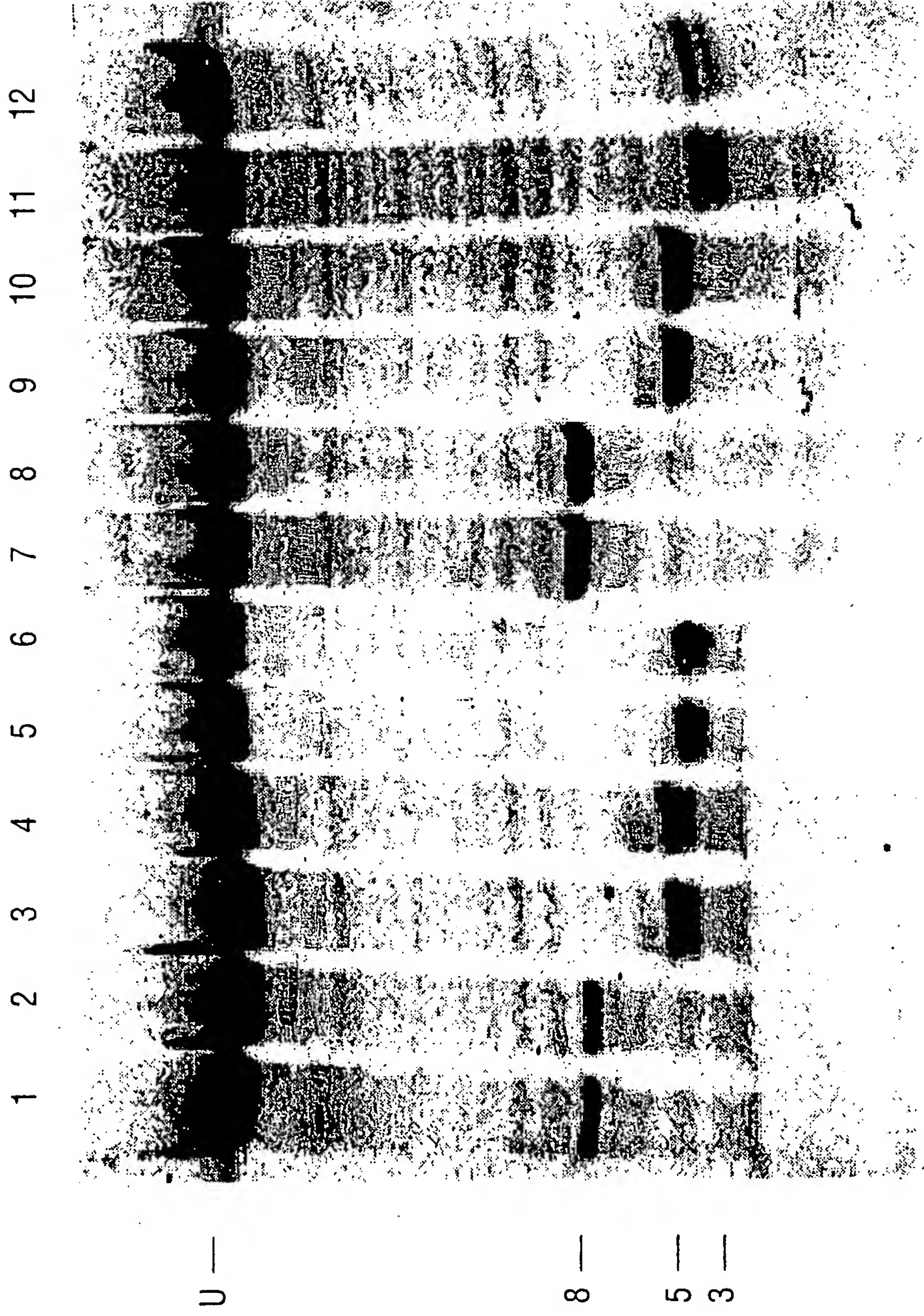


FIG. 69

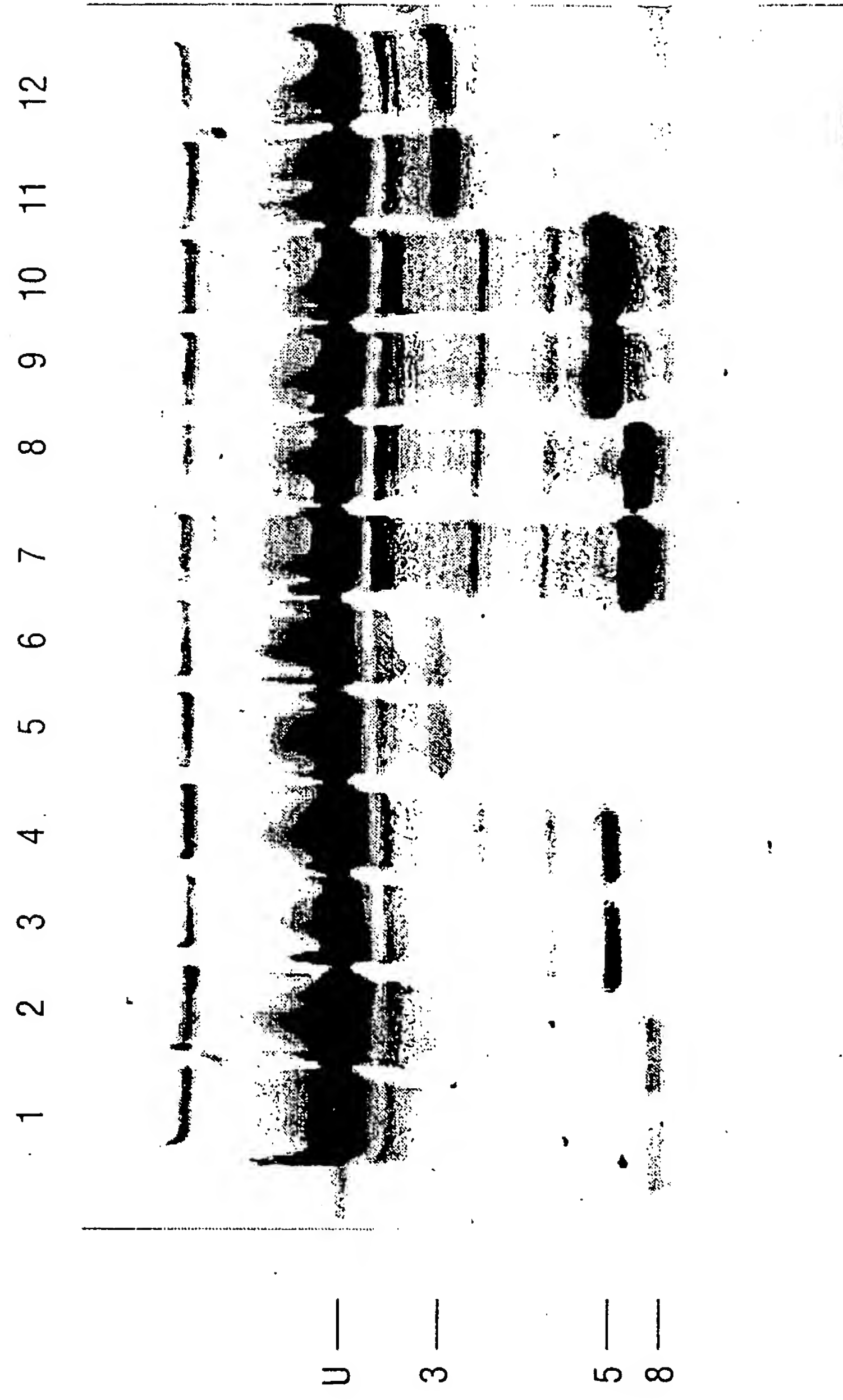
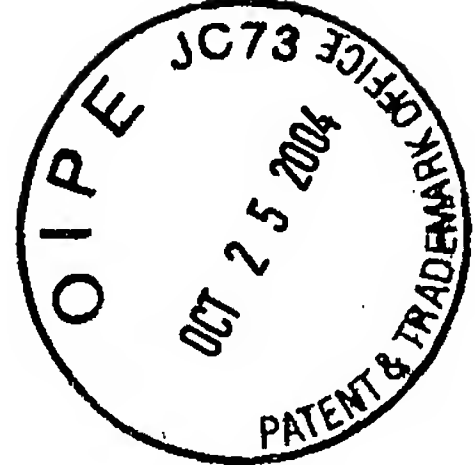
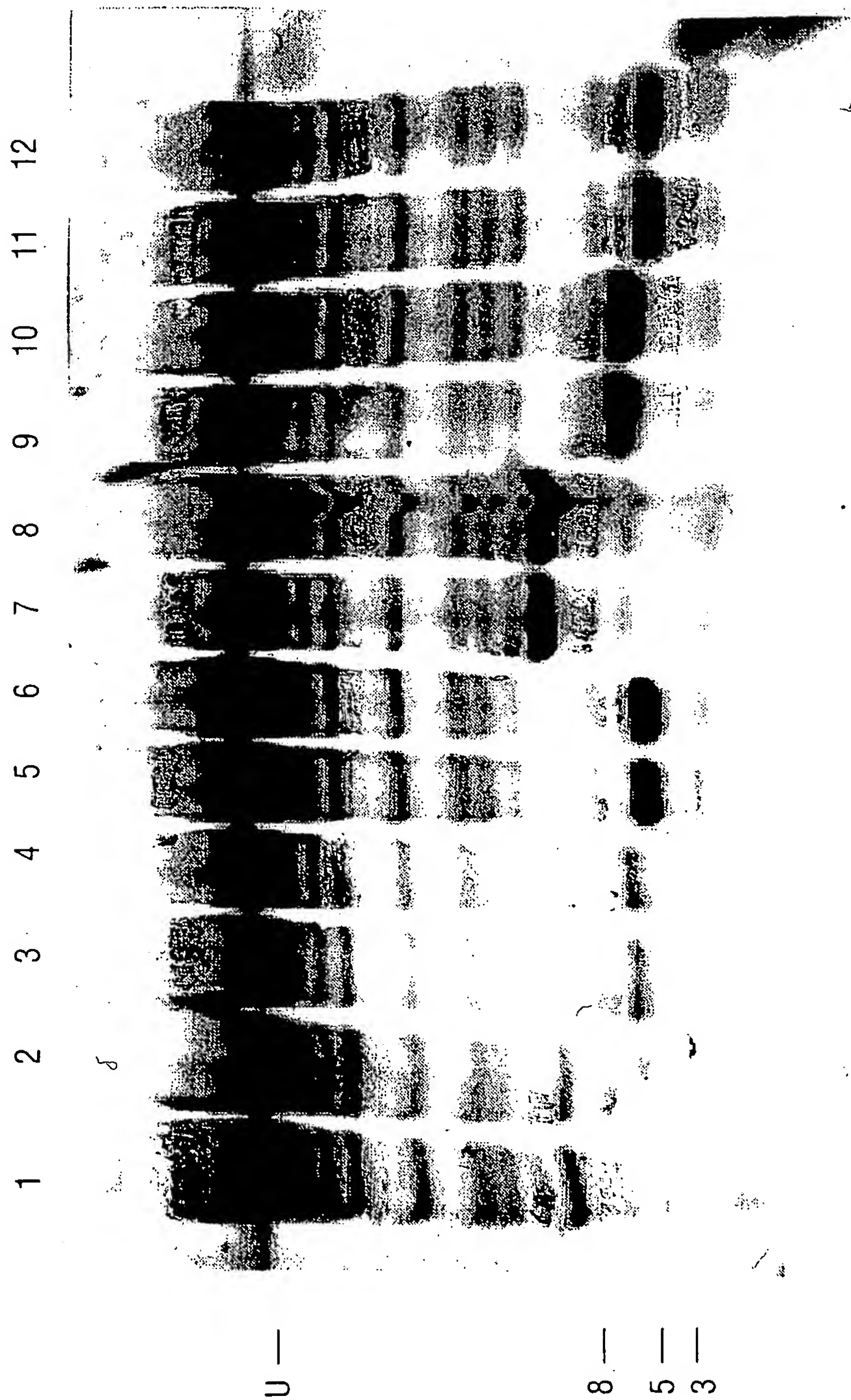
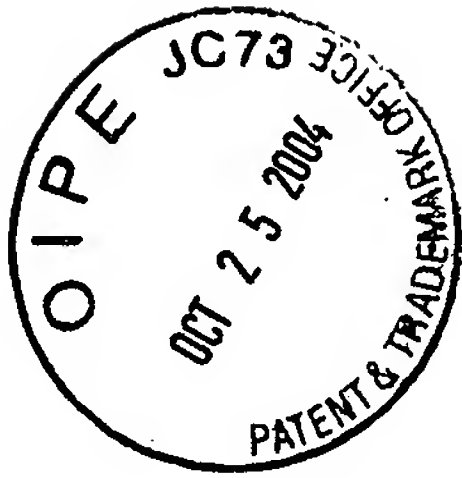


FIG. 70



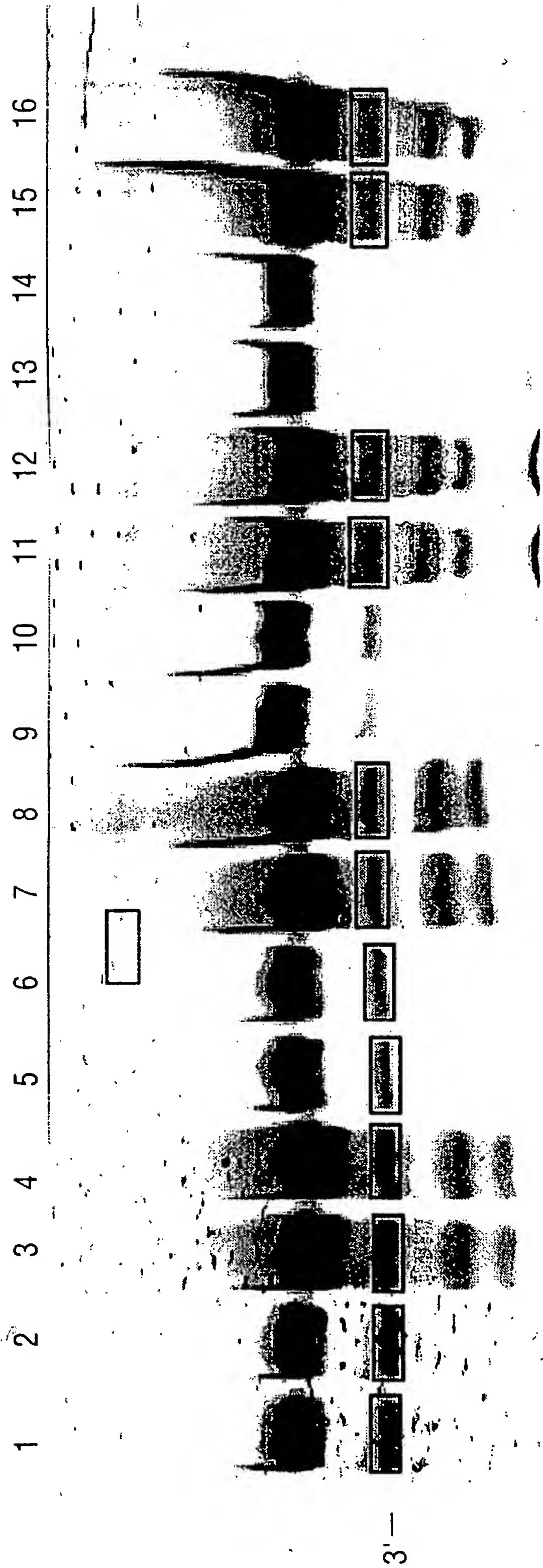


FIG. 72A

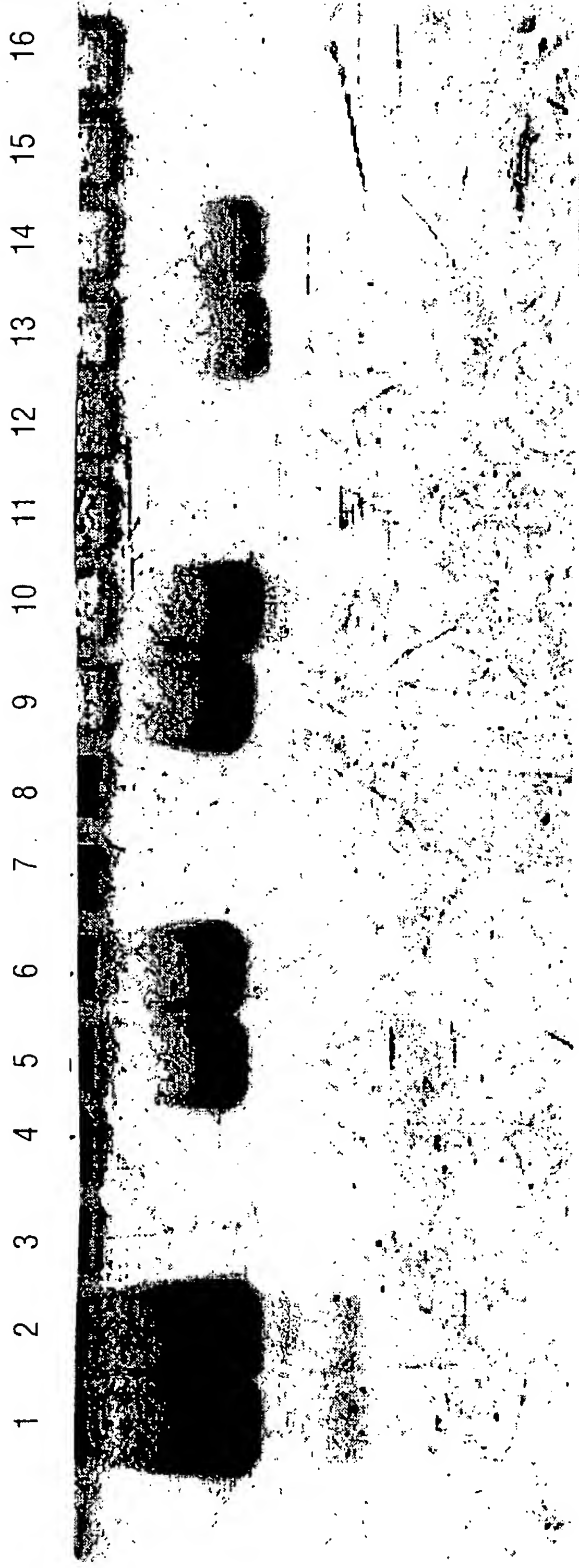
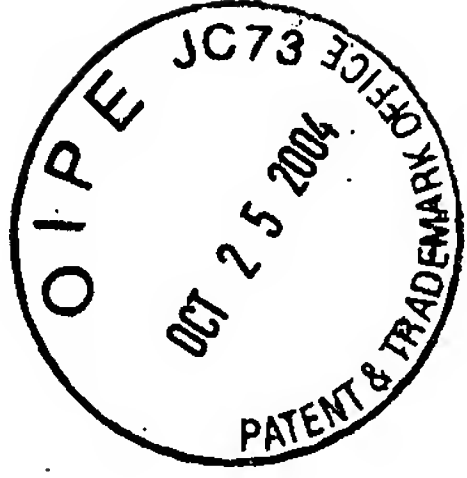


FIG. 72B

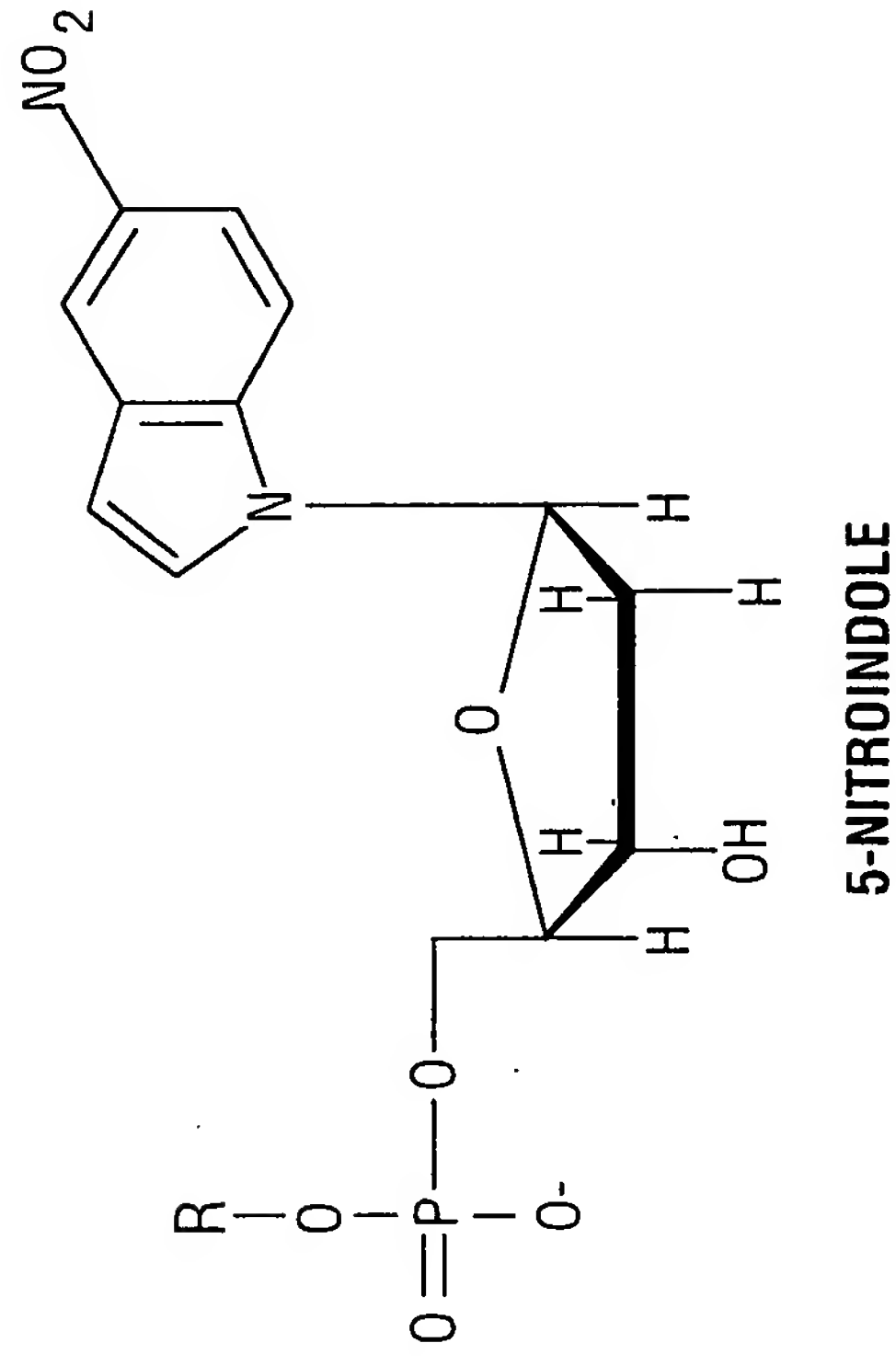
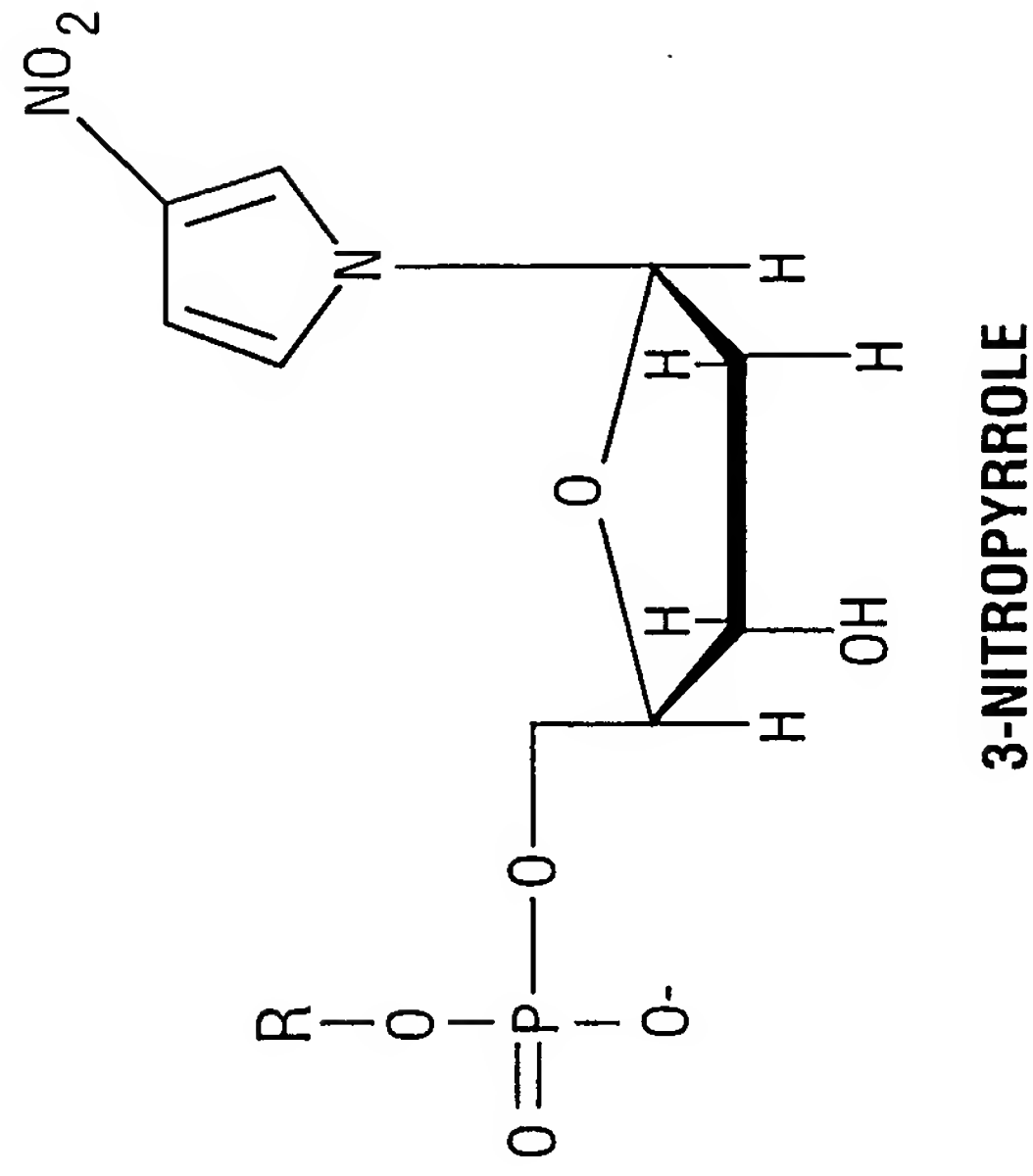
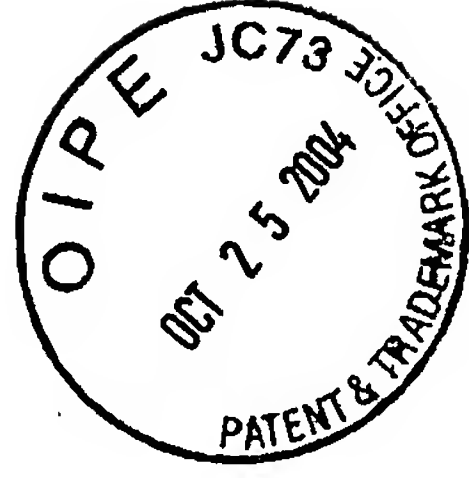
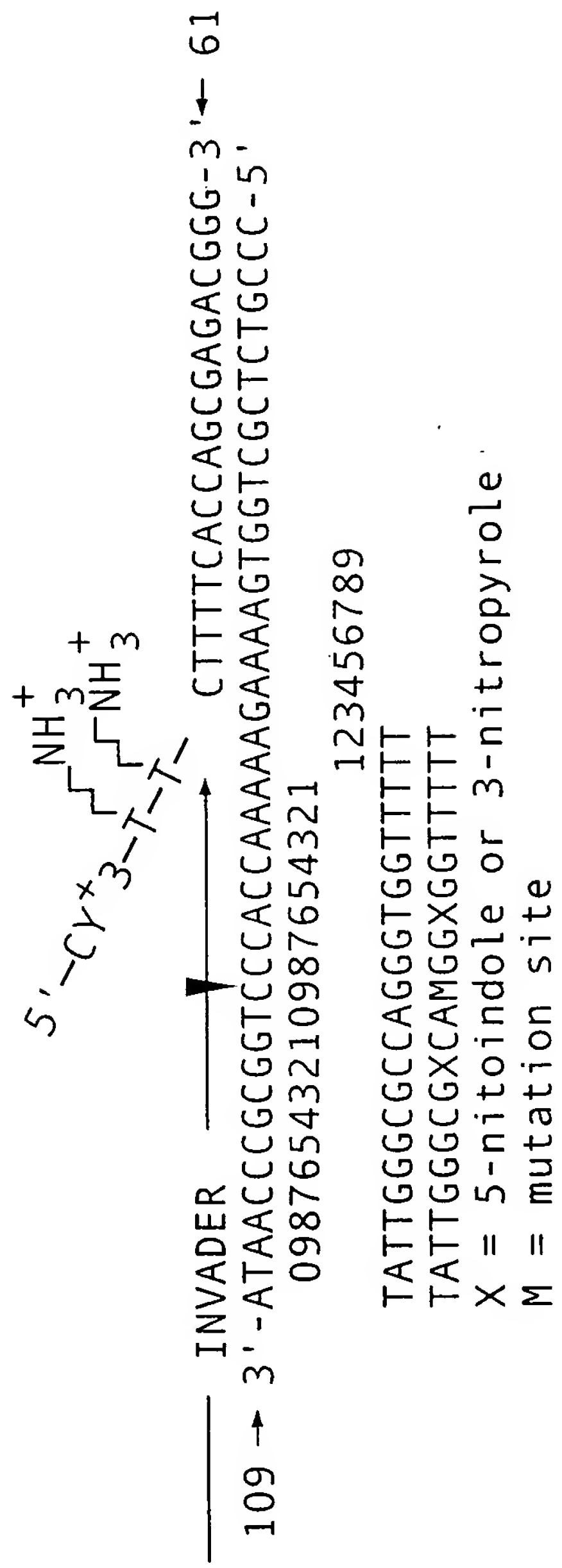


FIG. 73



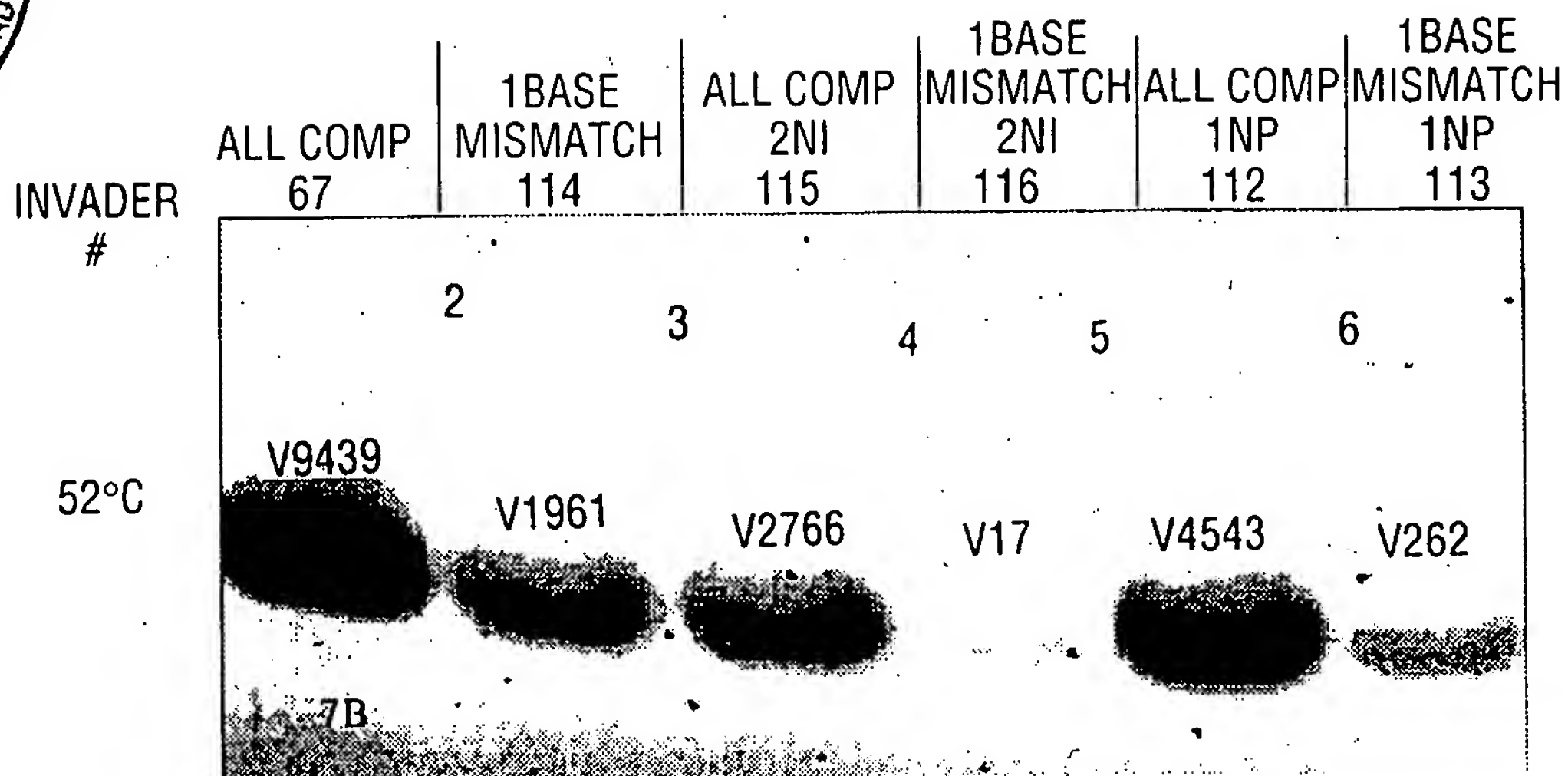
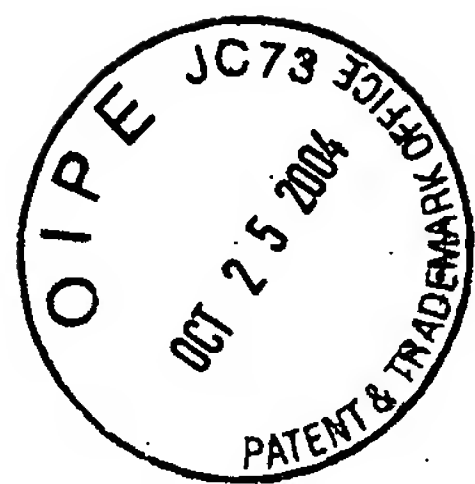


FIG. 75A

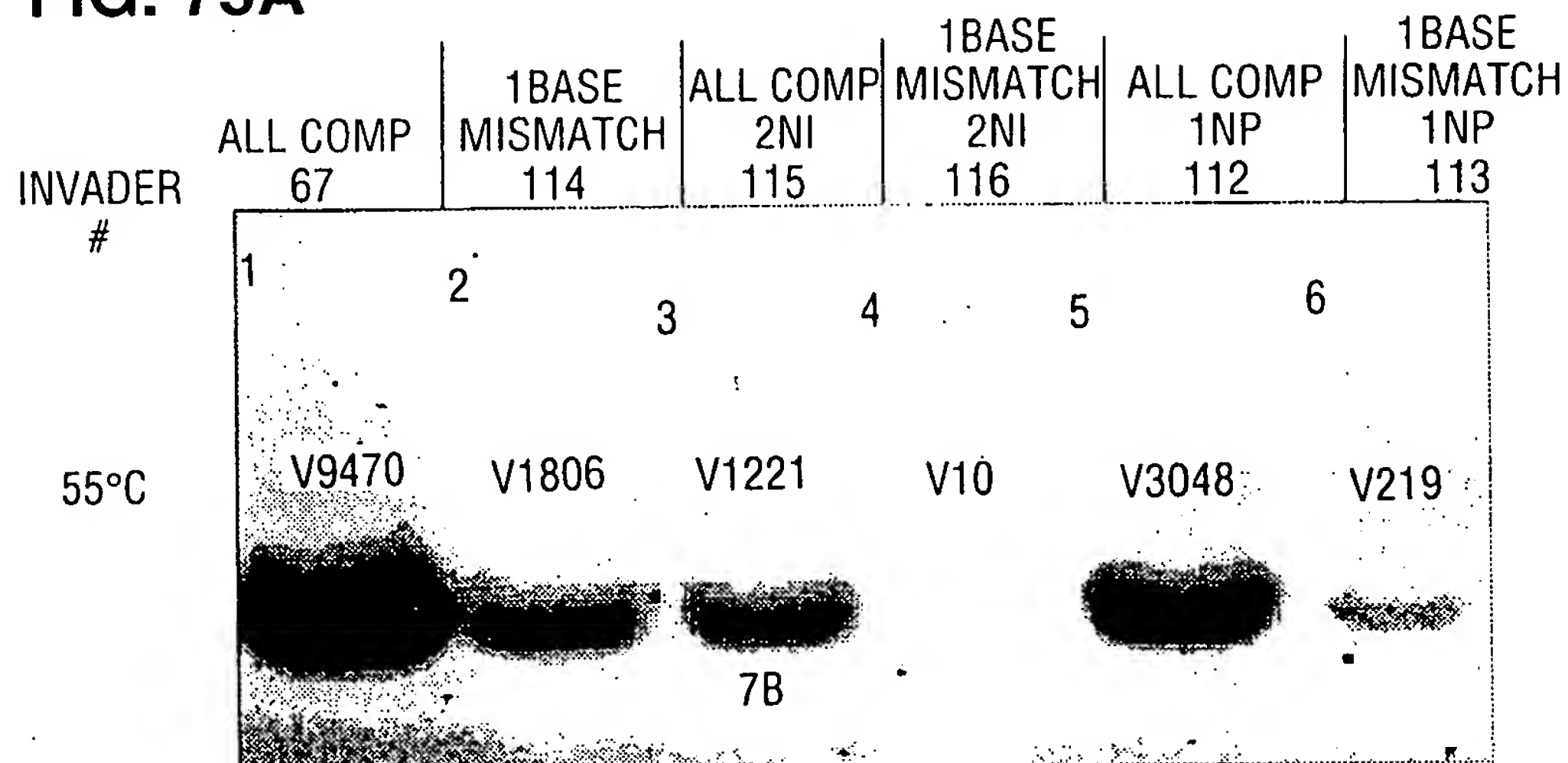
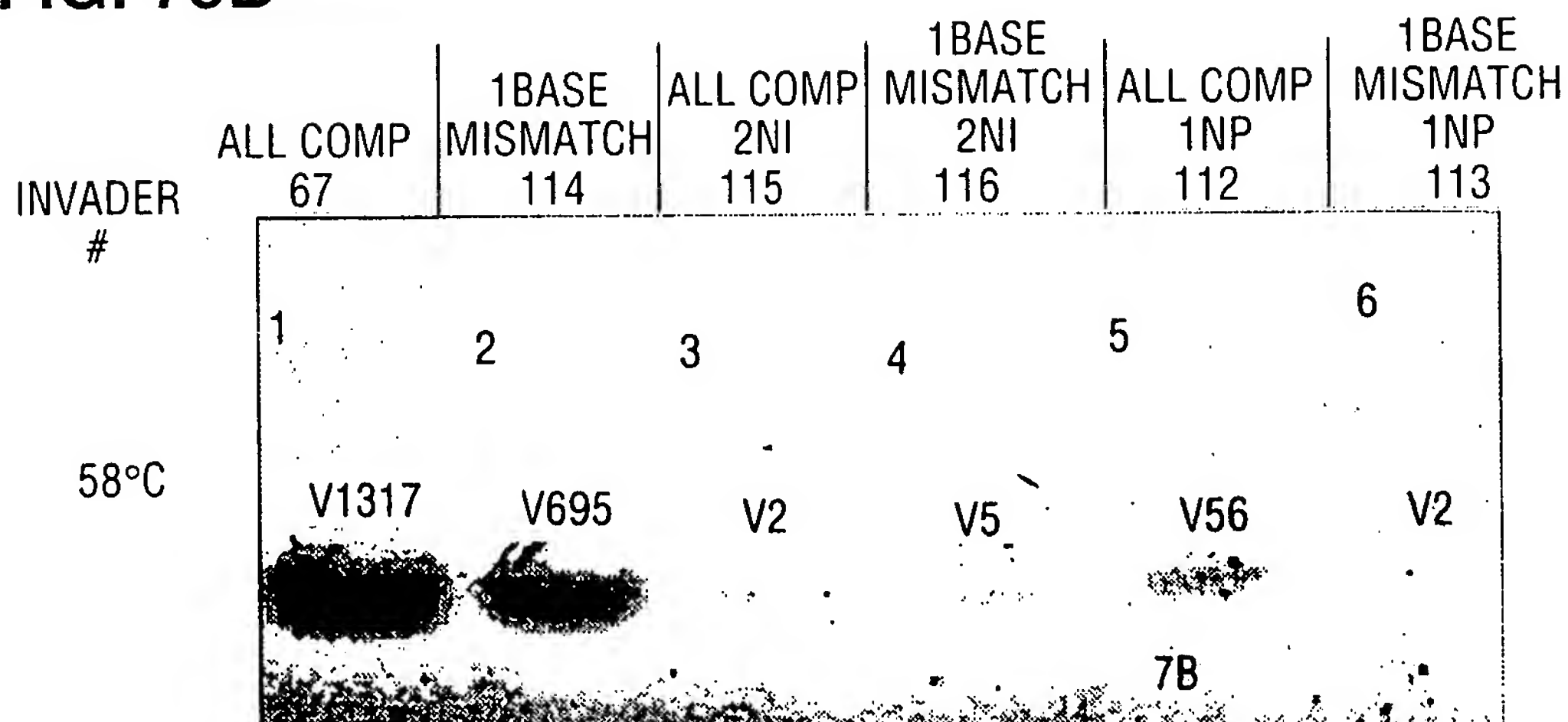


FIG. 75B



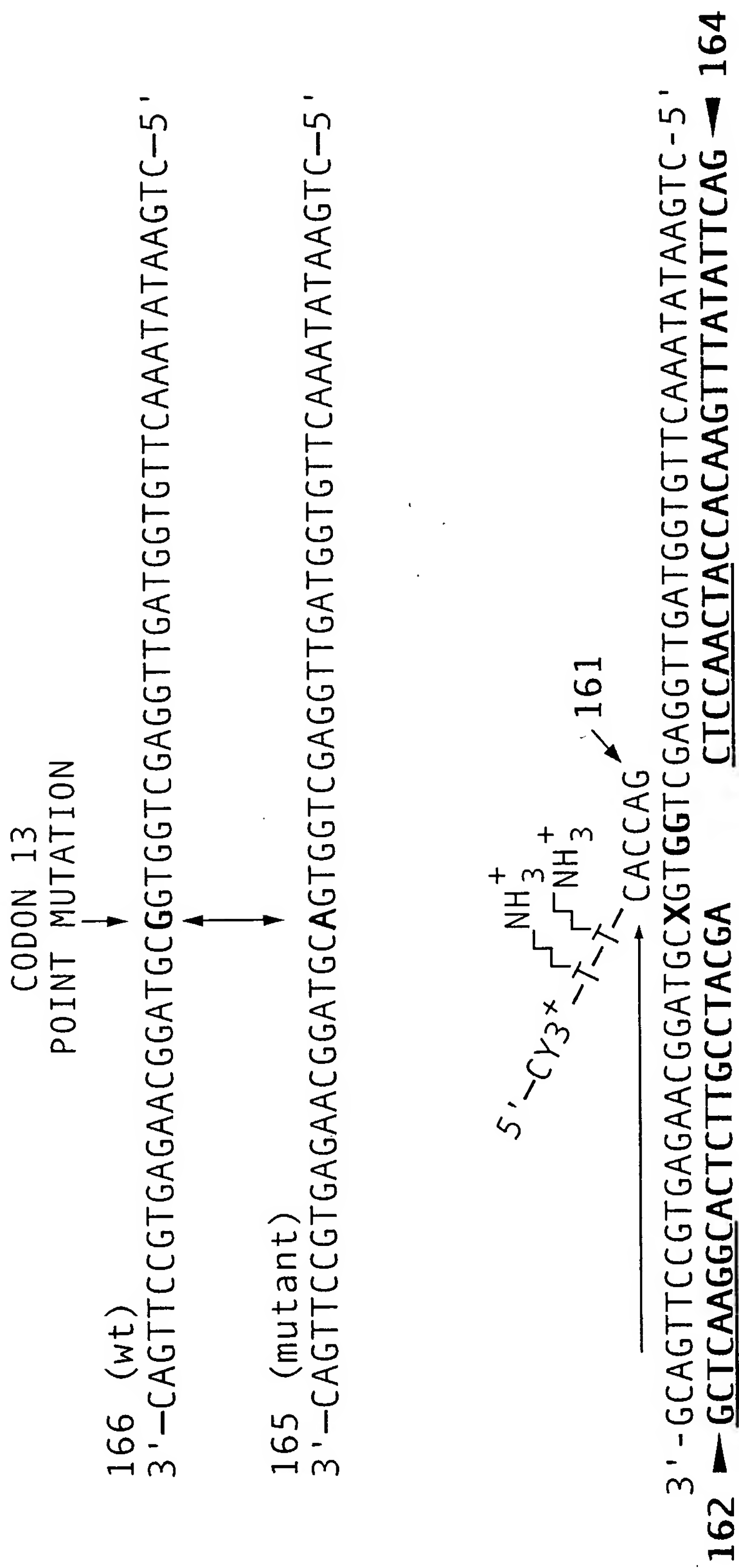
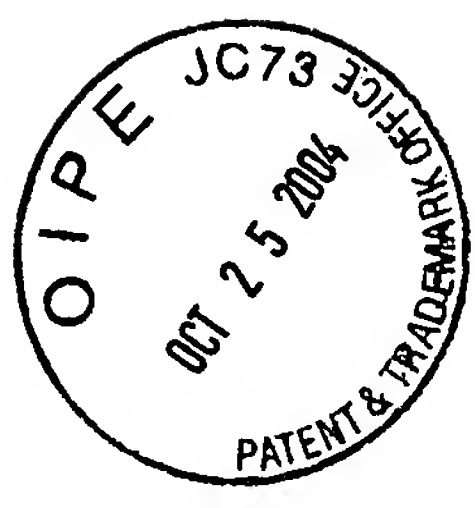


FIG. 76

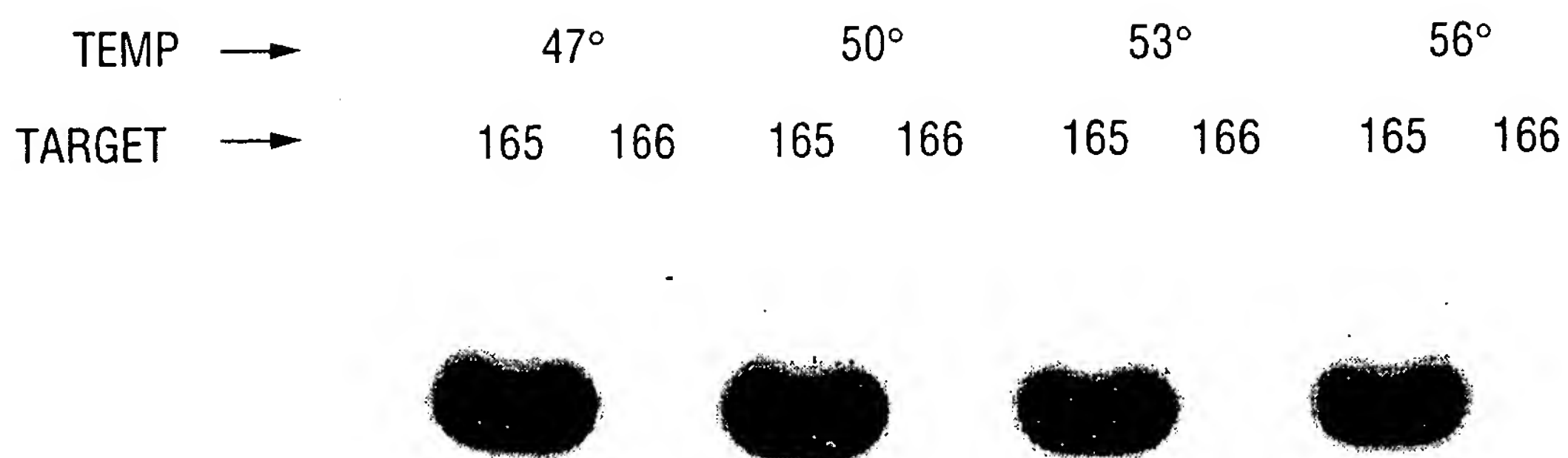
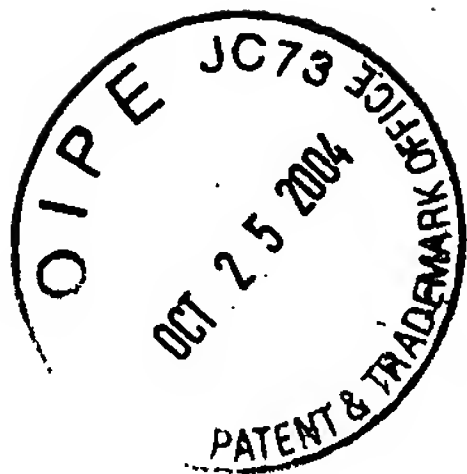
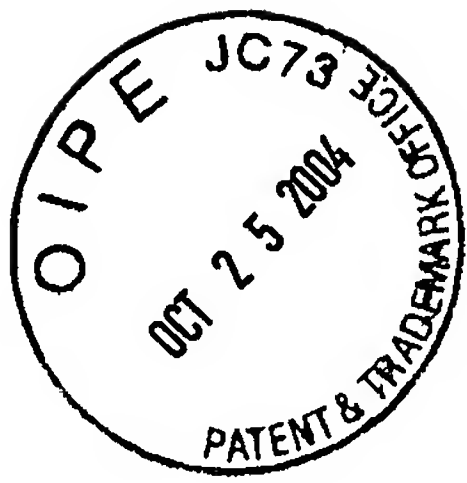


FIG. 77



F1
5' GTTCTCTGCTCTCTGGT 1819
CGCTGTCTCGCTTGT^G
GCGACAGAGCGAACA^A
3' GCTCTCTGGT

FIG. 78A

F1
5' GTTCTCTGCTCTCTGGT 2122
CGCT GTCTCGCTTGT^G
3' GCTCTCTGGTGCGACAGAGCGAACA^A
5' CGAGAGACCGCT^G
P15

FIG. 78B

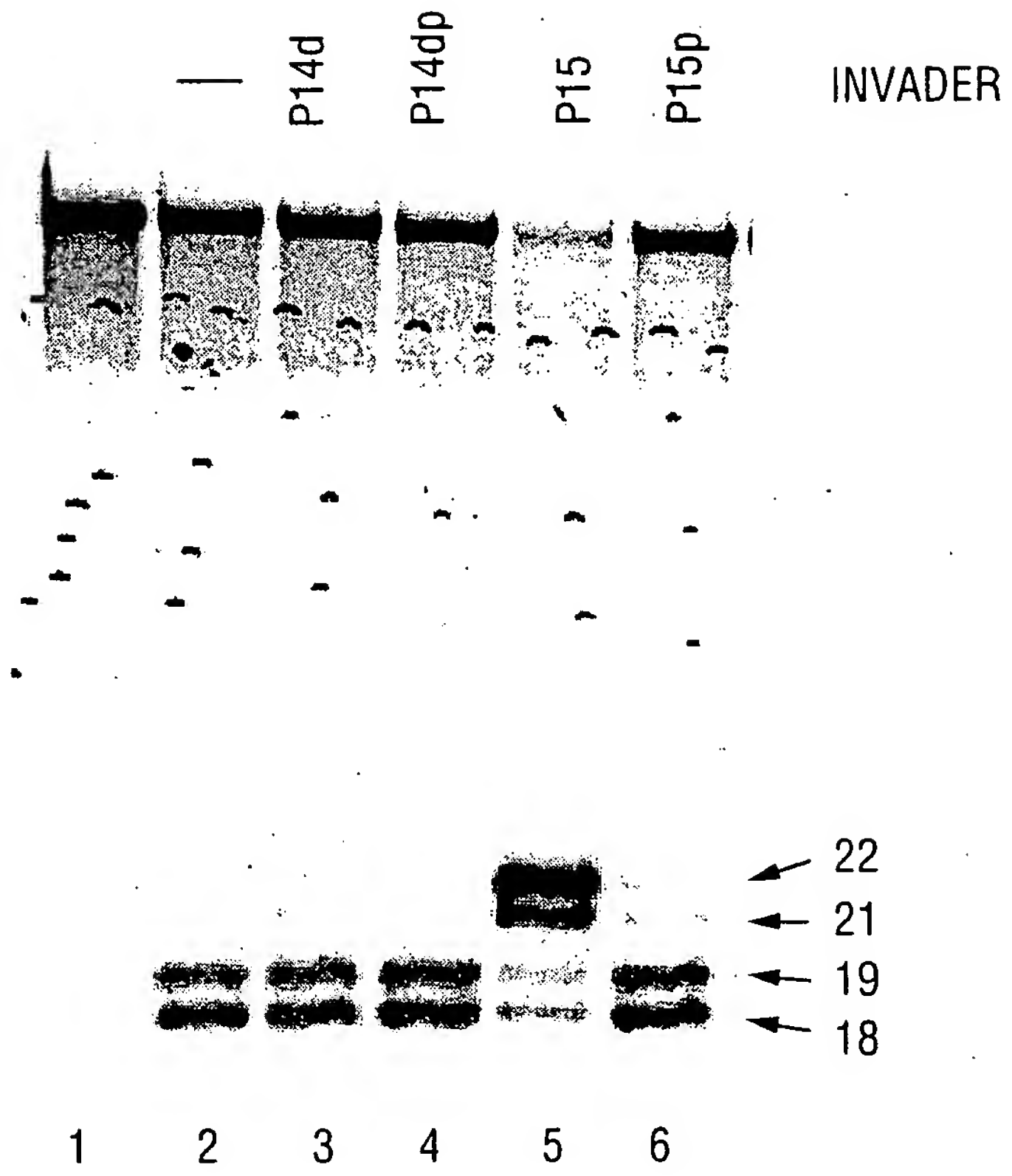


FIG. 78C

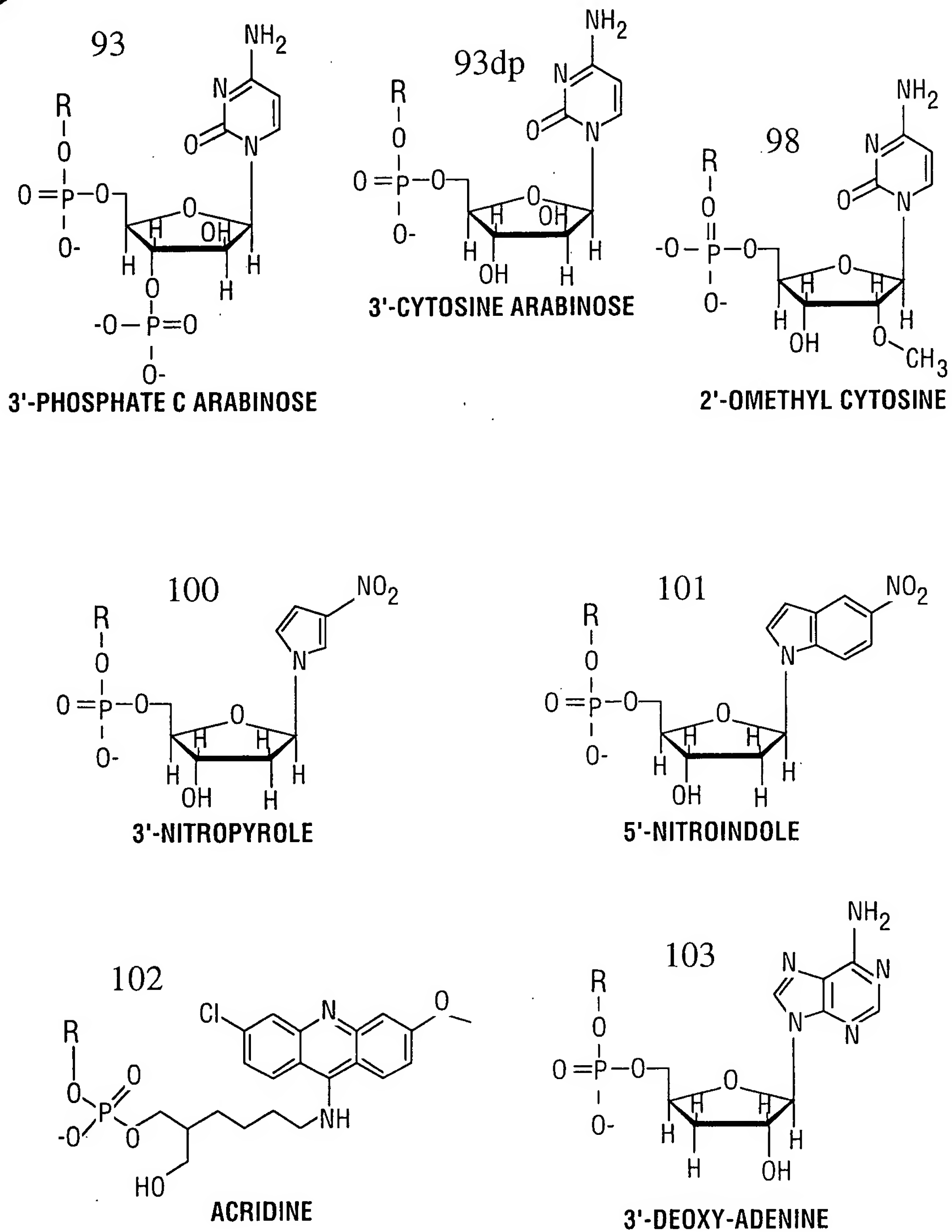
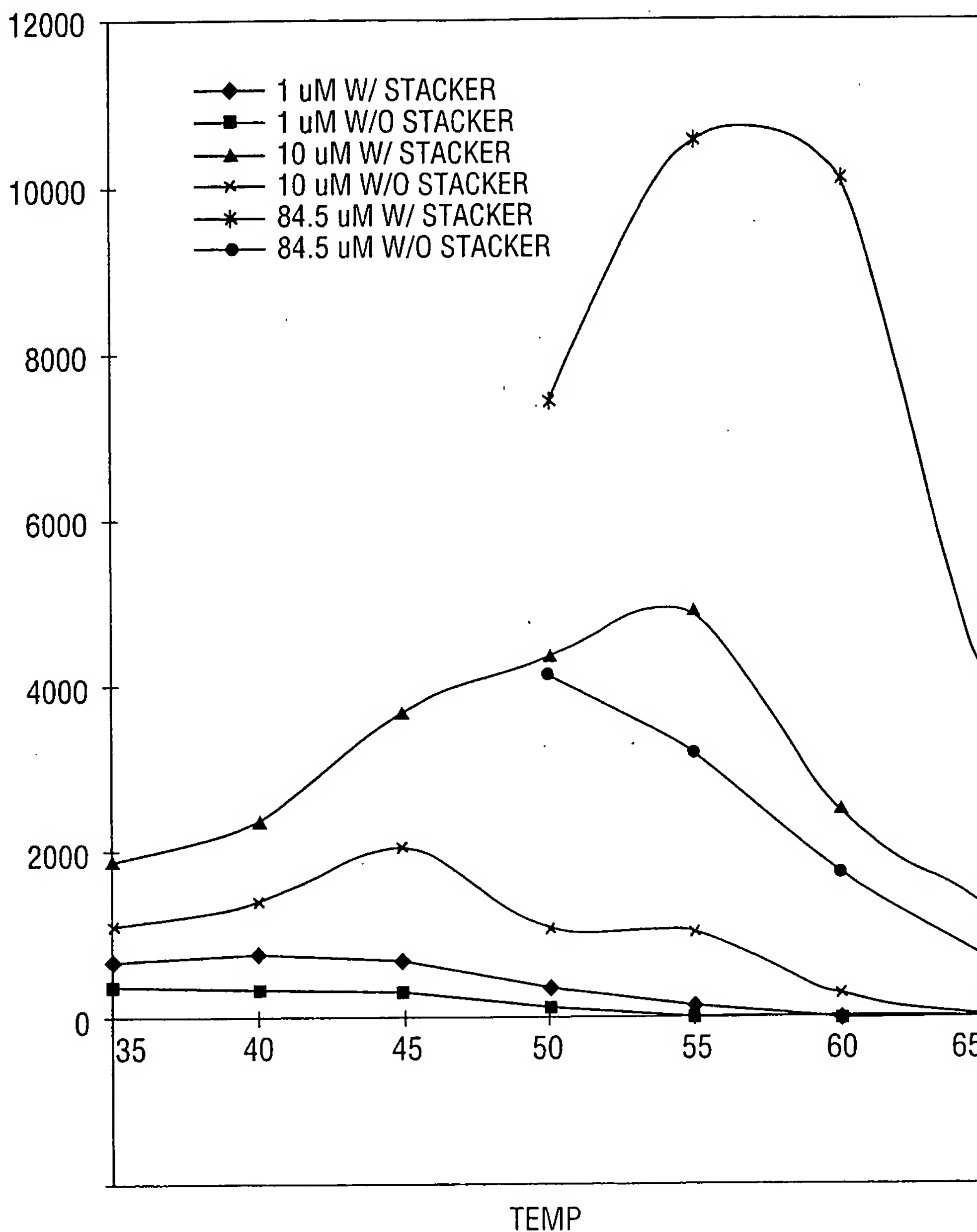


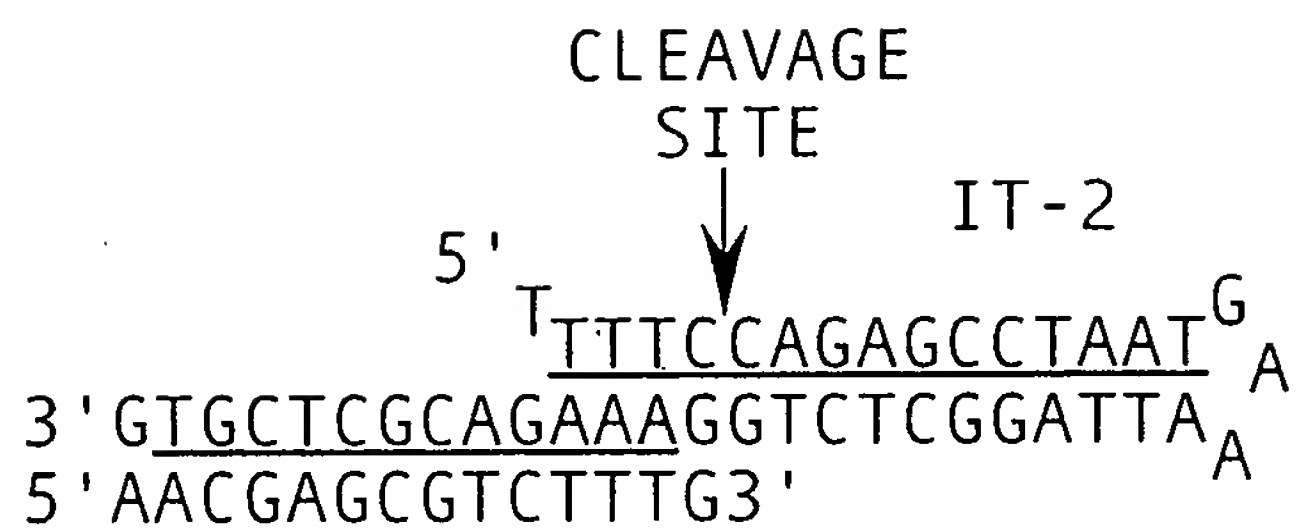
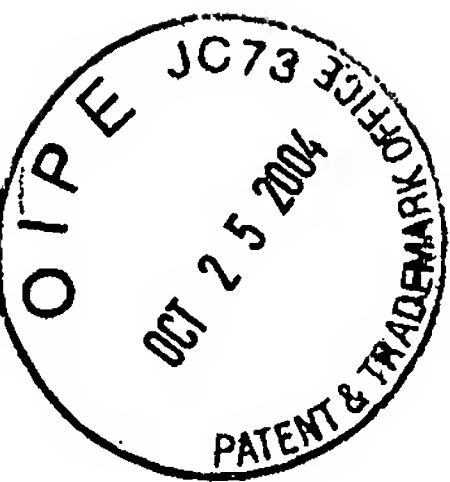
FIG. 79

COUNTS

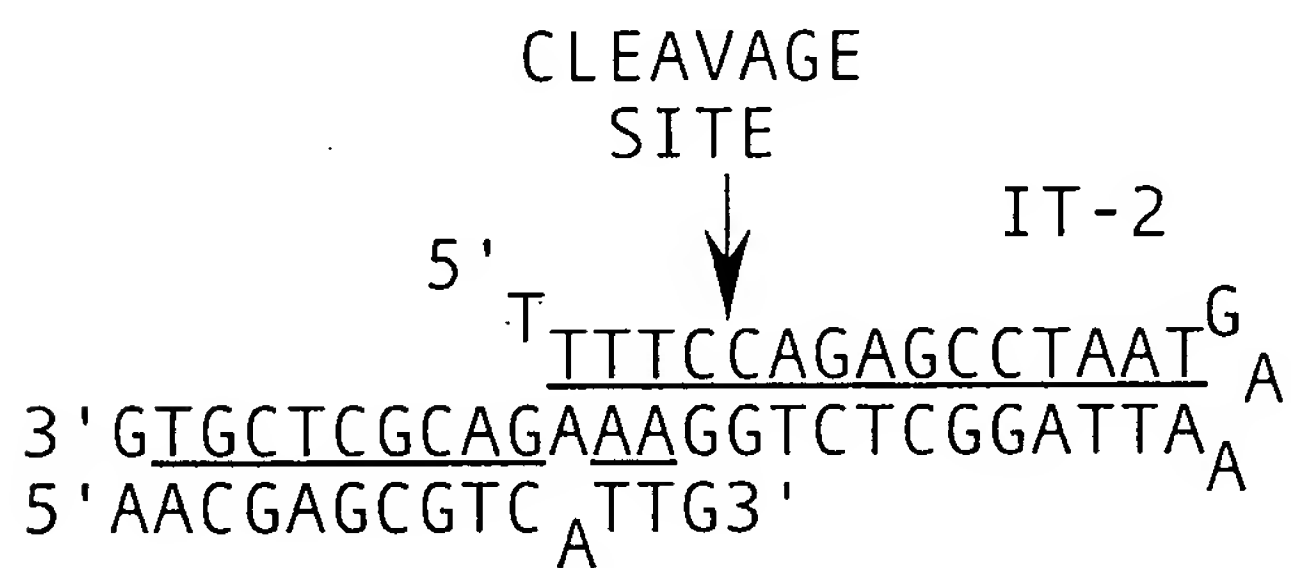


CONCENTRATION OF PROBE W/ AND W/O STACKER vs TEMP

FIG. 80



IT-1



IT-1A4

FIG. 81

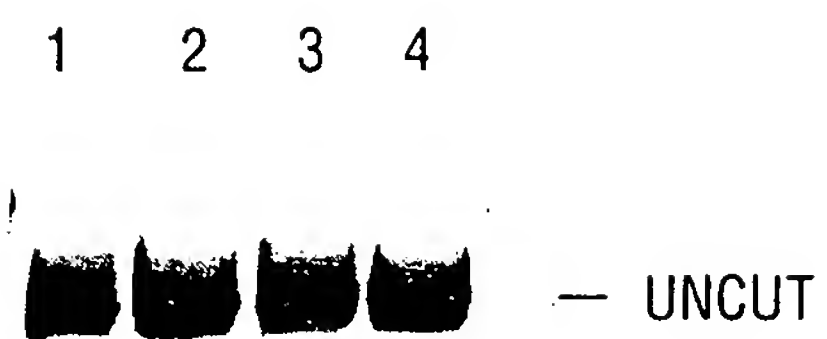
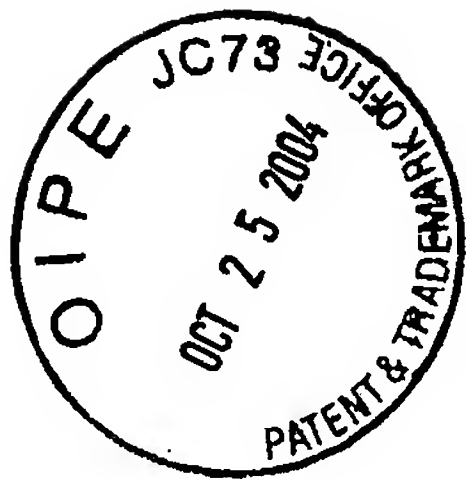


FIG. 82

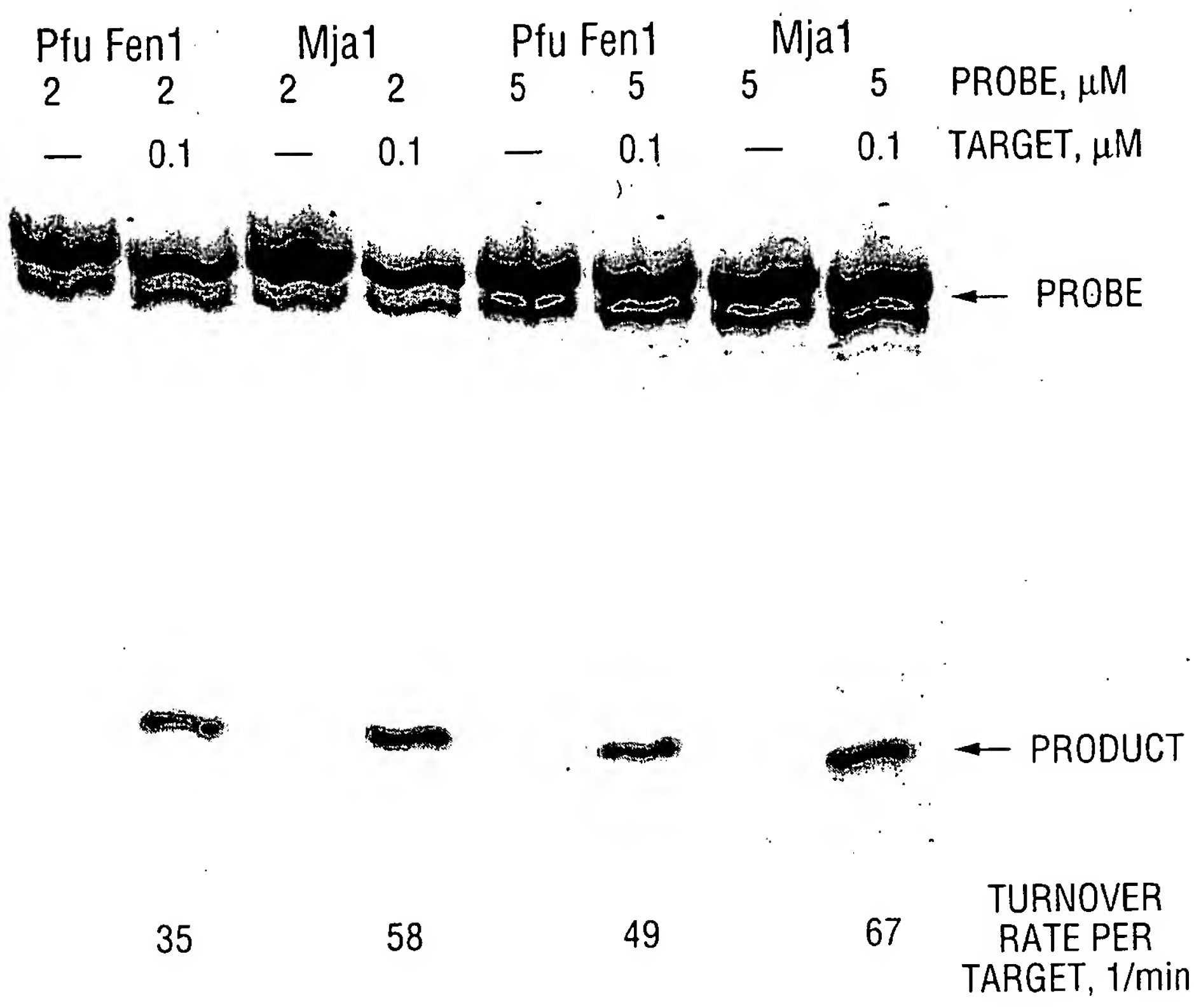
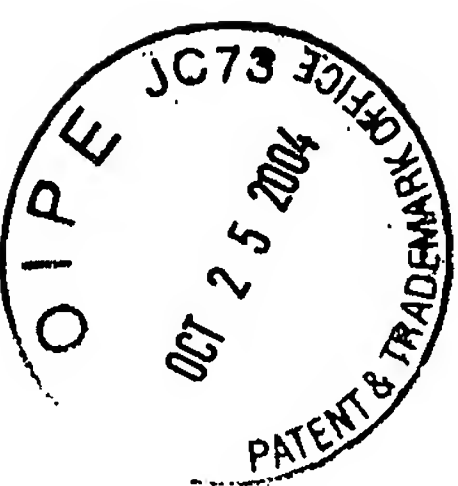


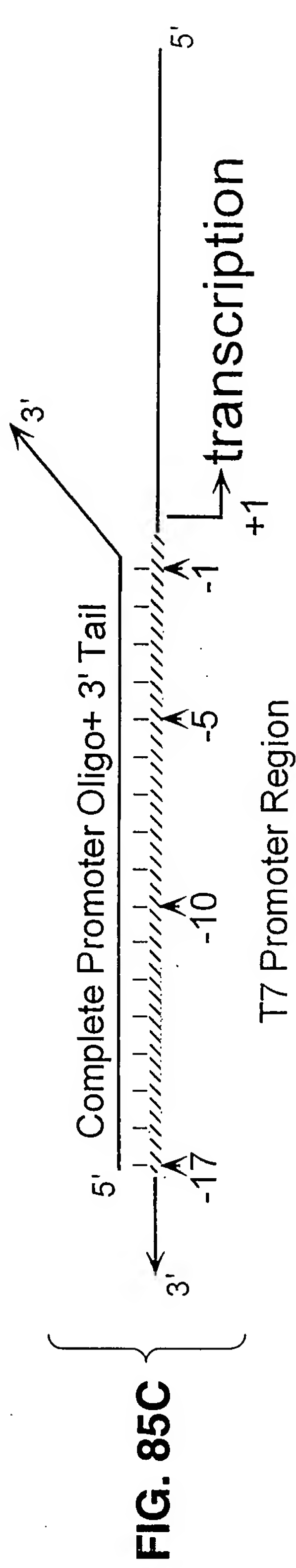
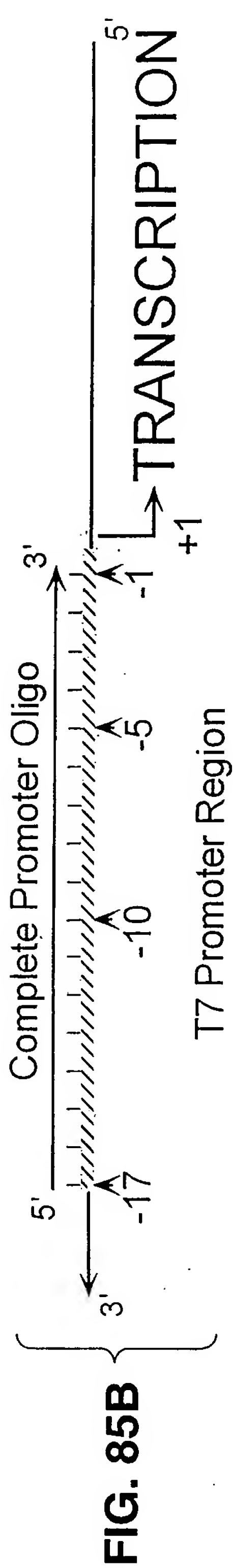
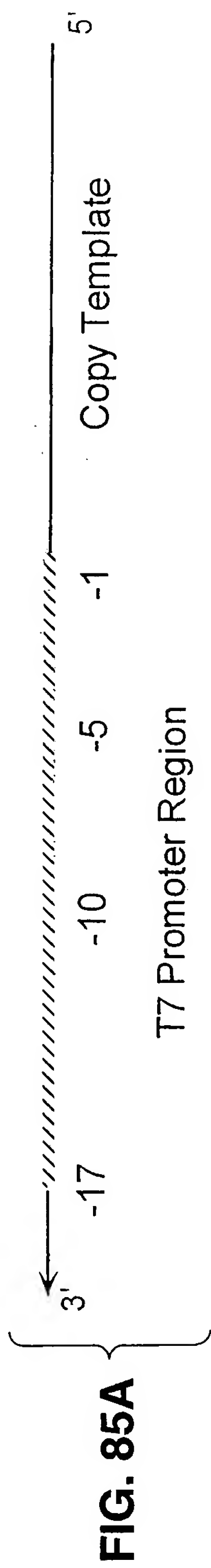
FIG. 83

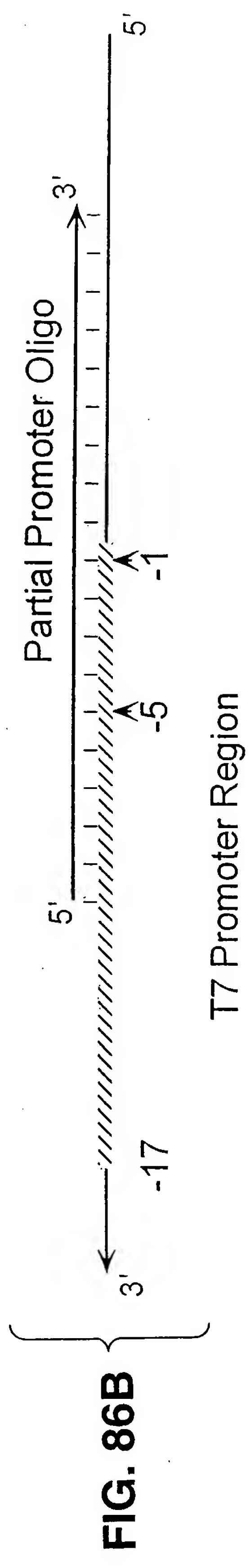
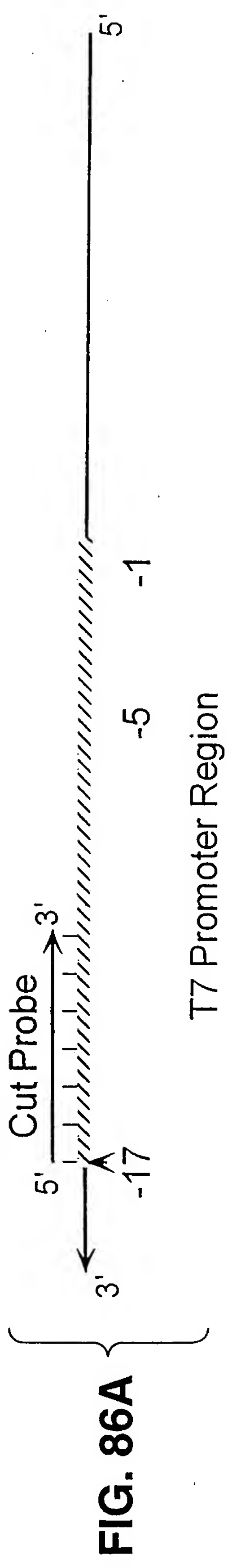
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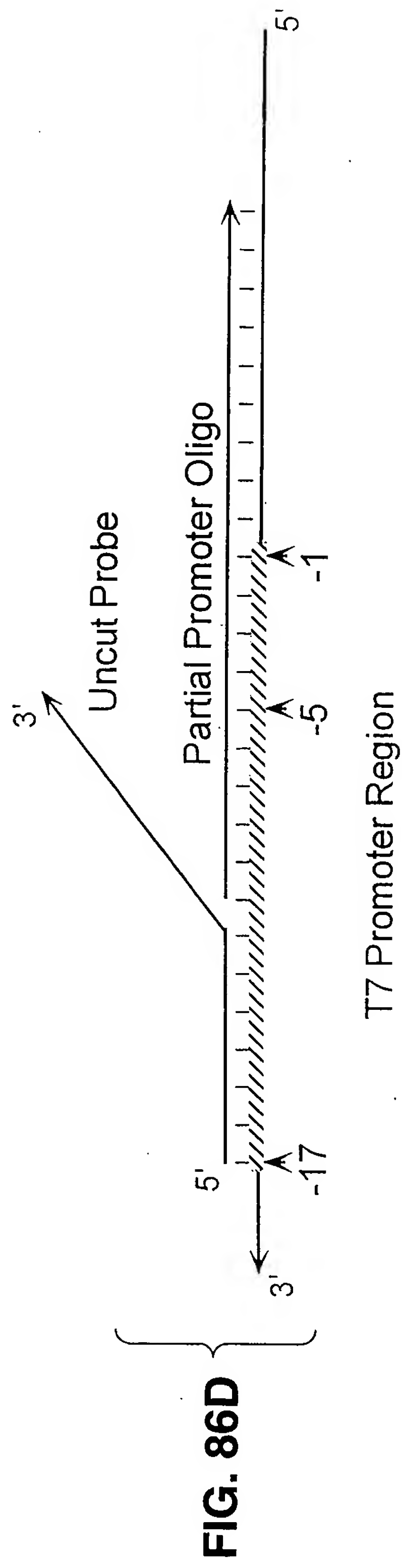
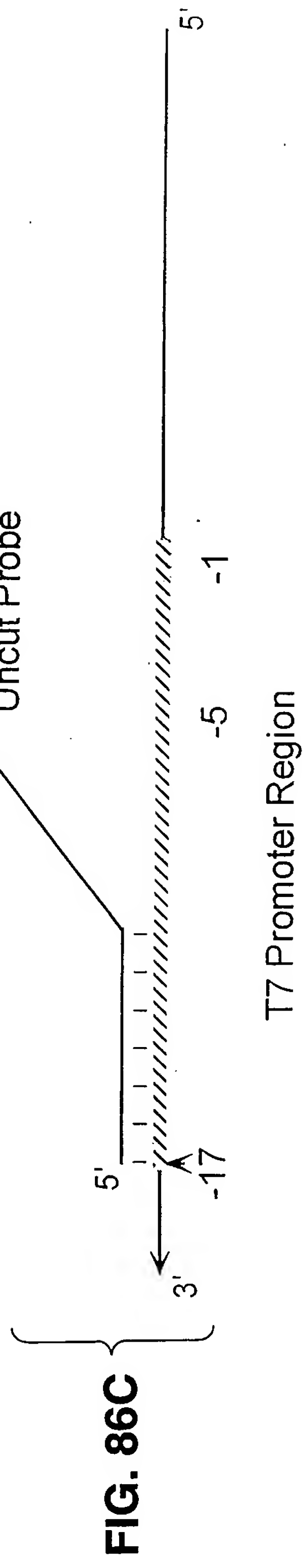
1 2 3 4 5



FIG. 84







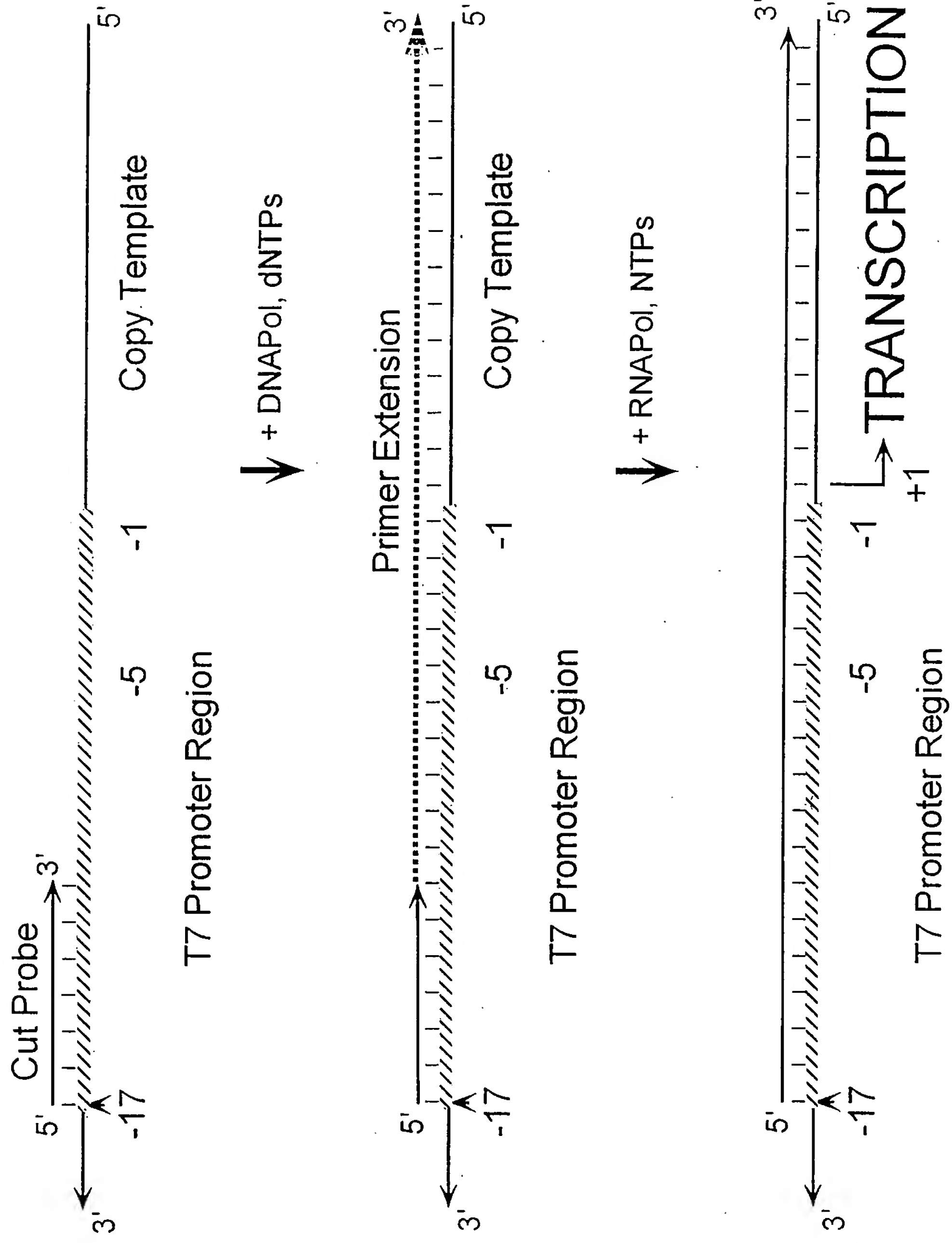
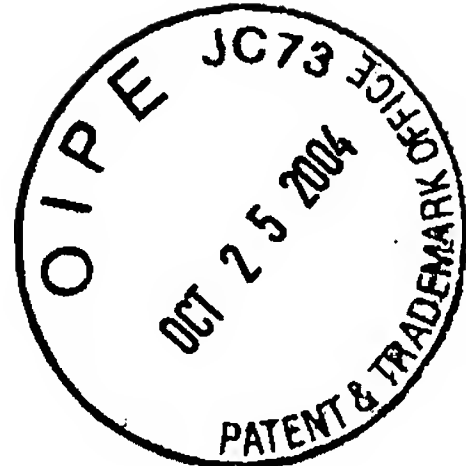
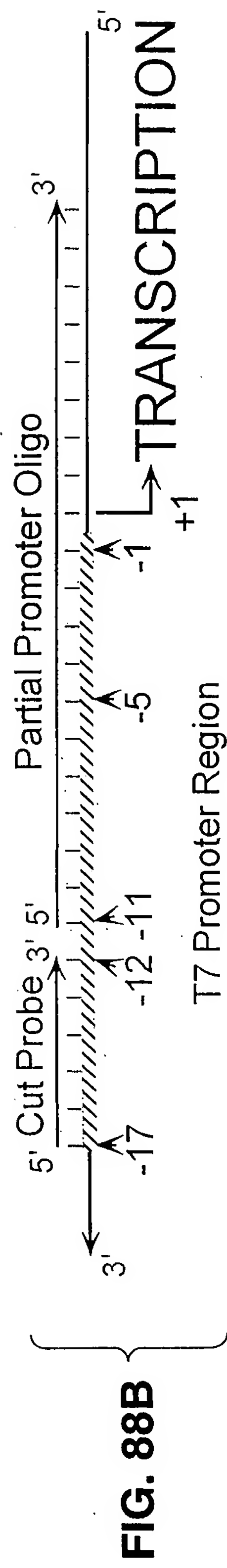
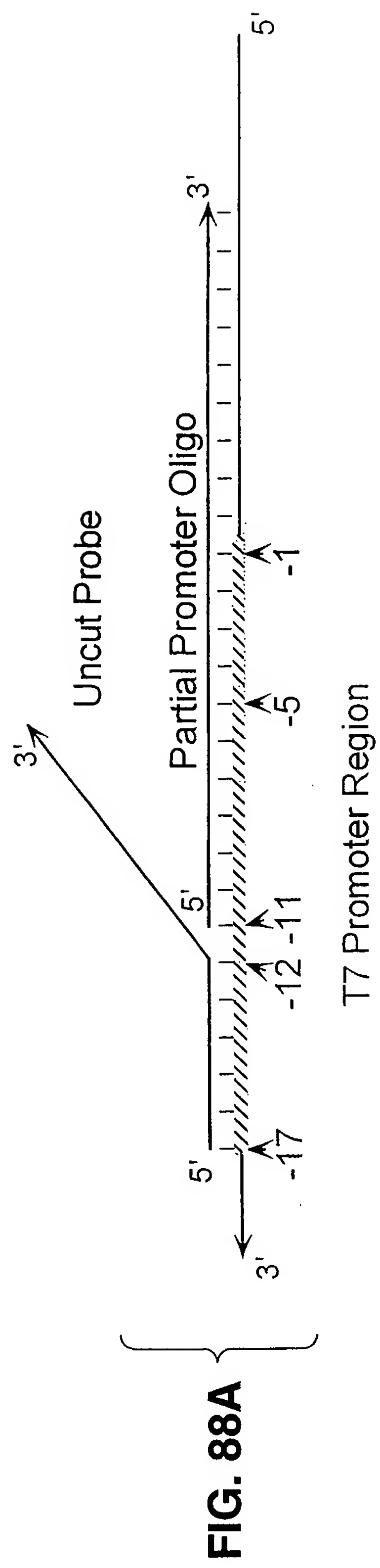


FIG. 87



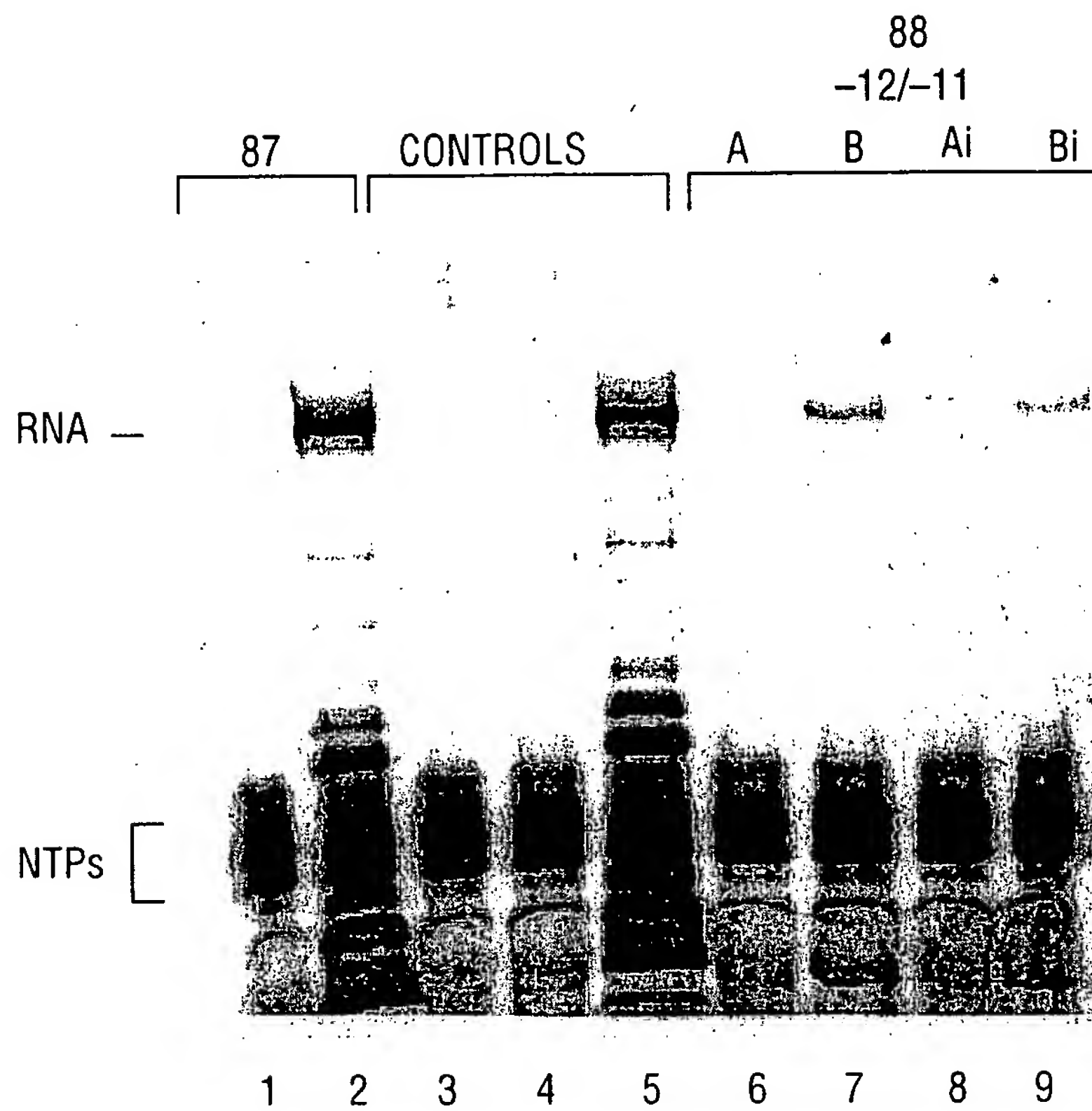
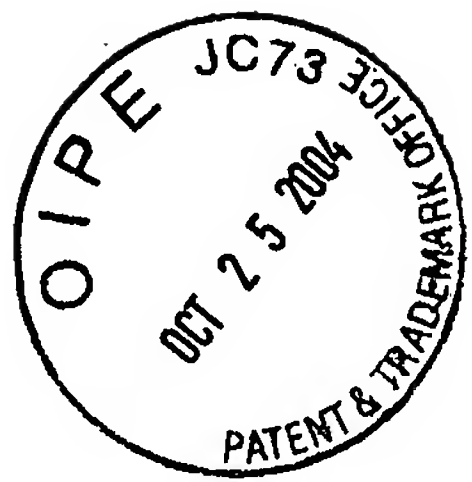
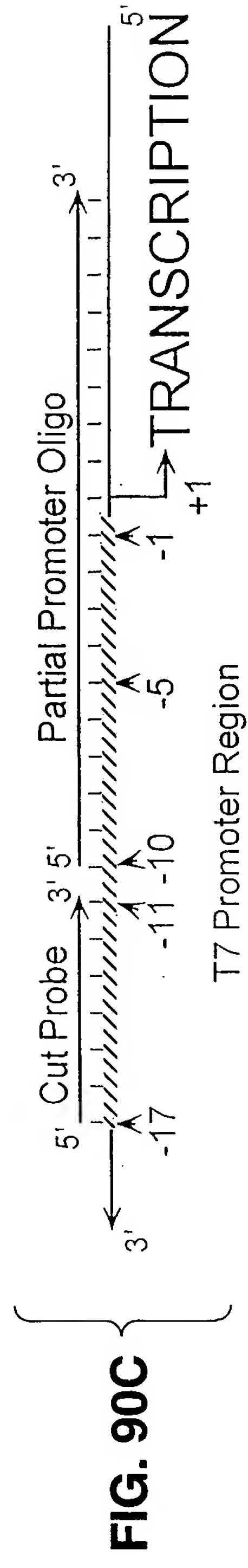
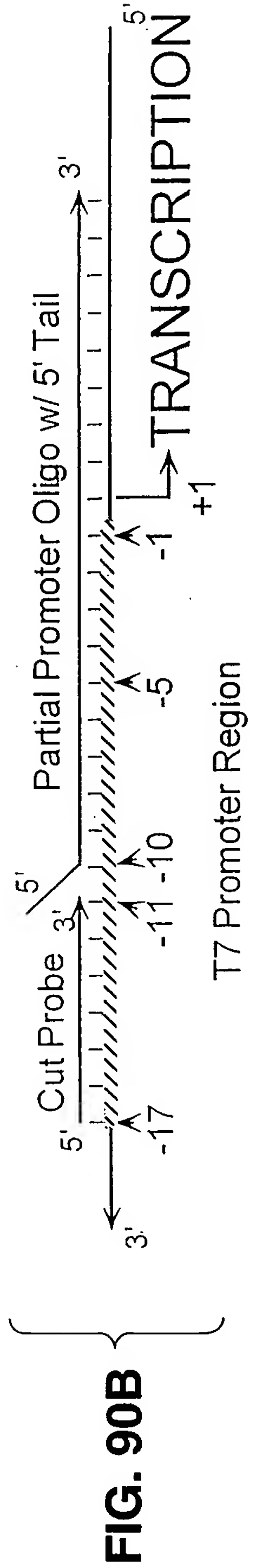
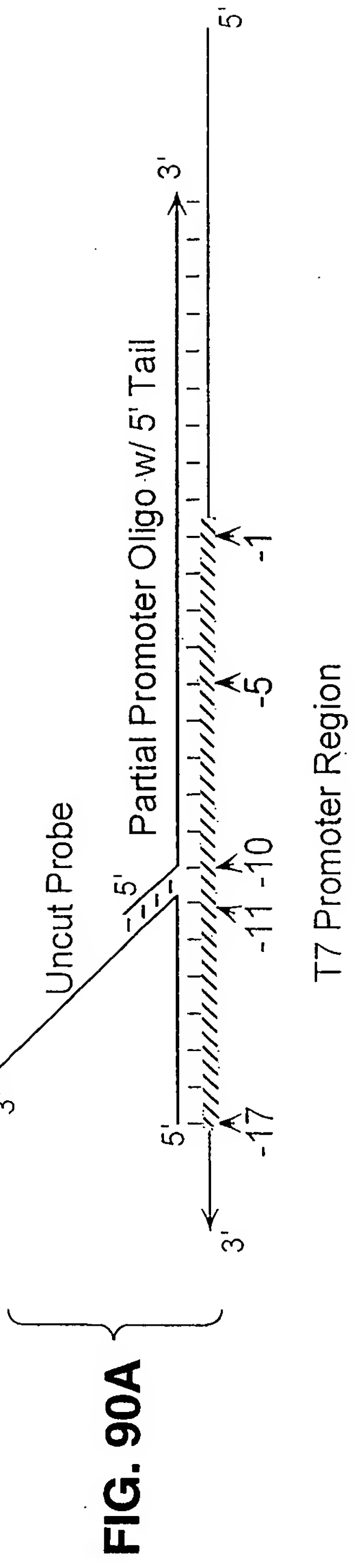


FIG. 89



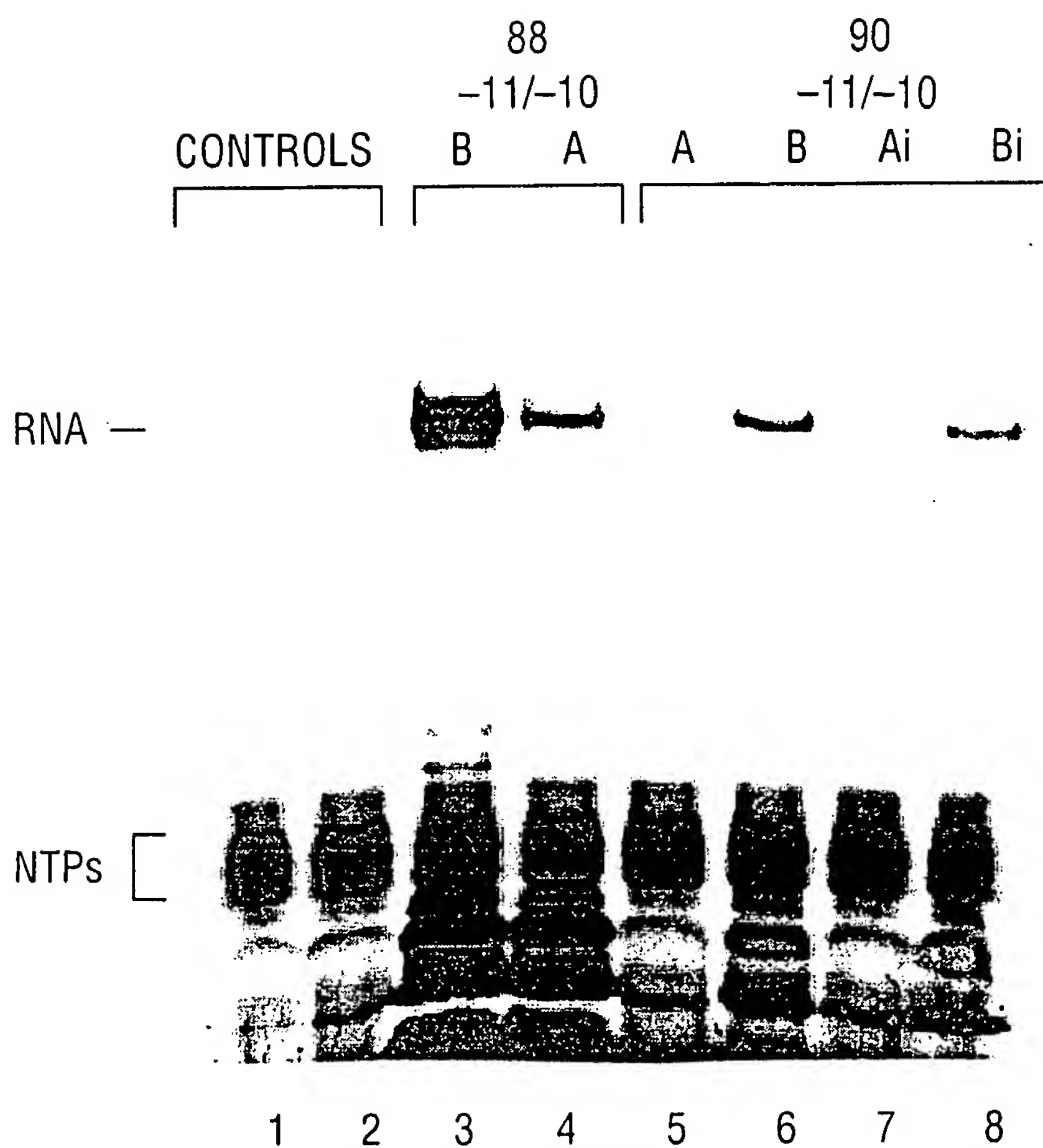
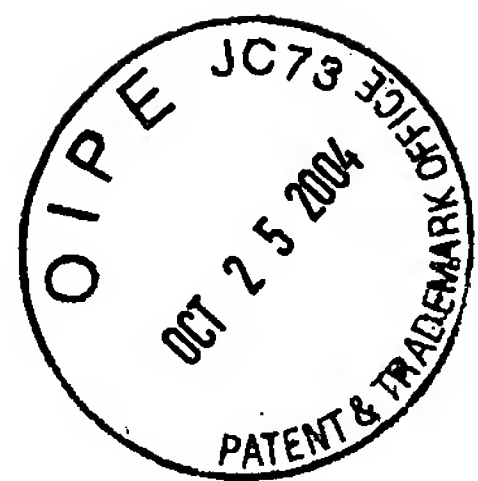


FIG. 91

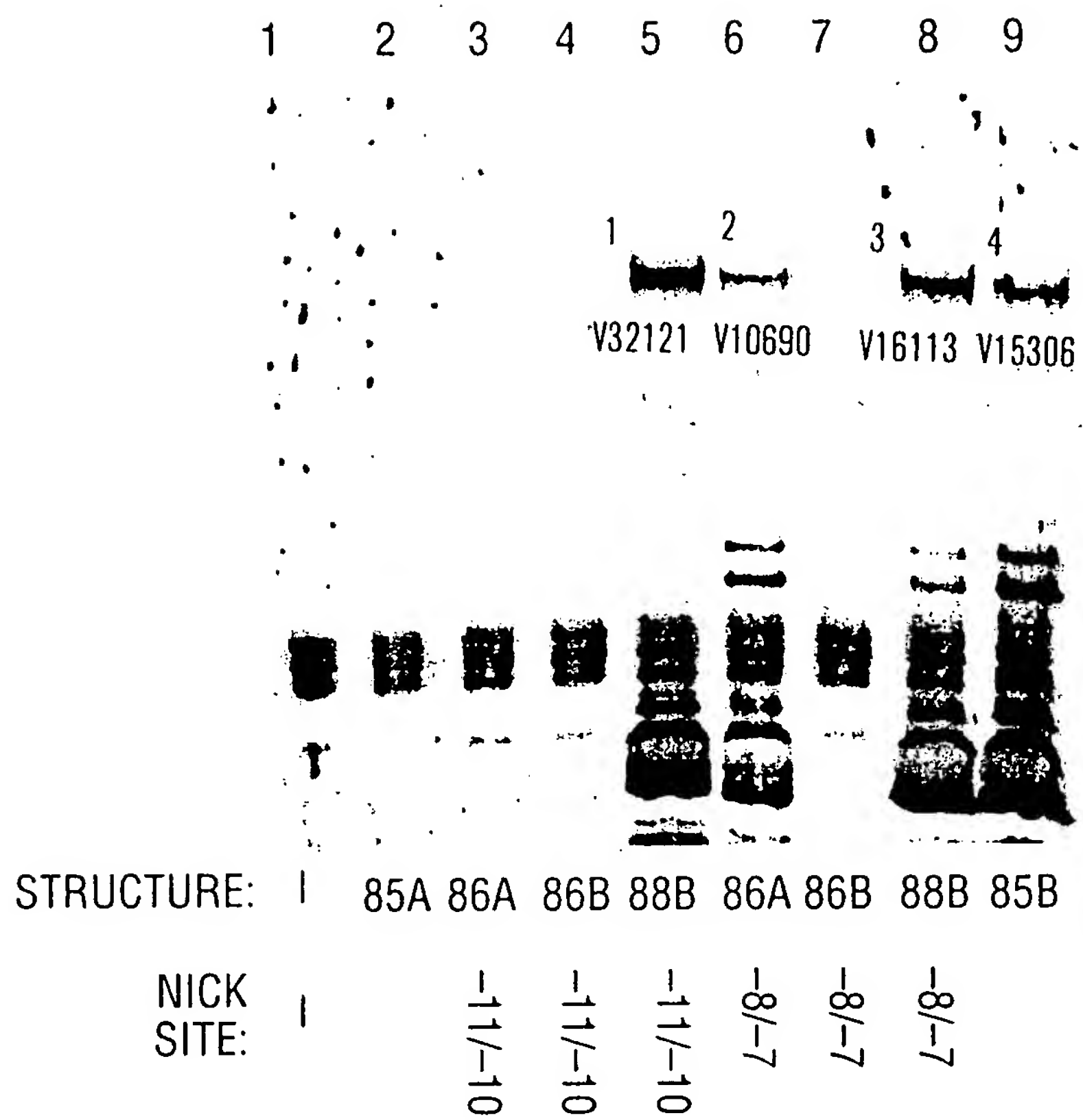
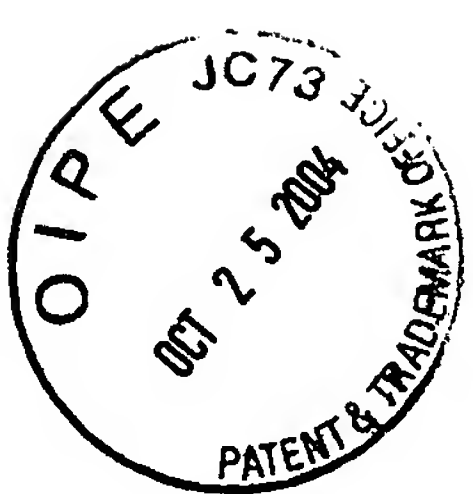


FIG. 92

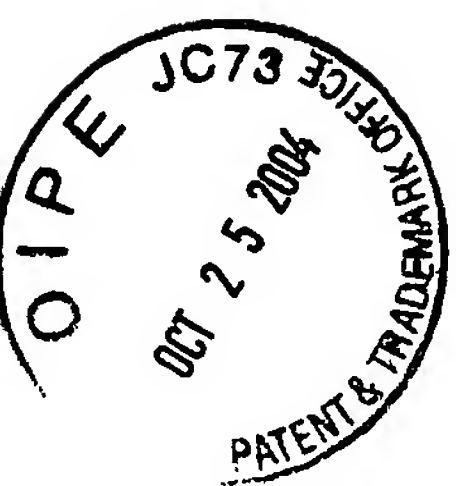


FIG. 93A

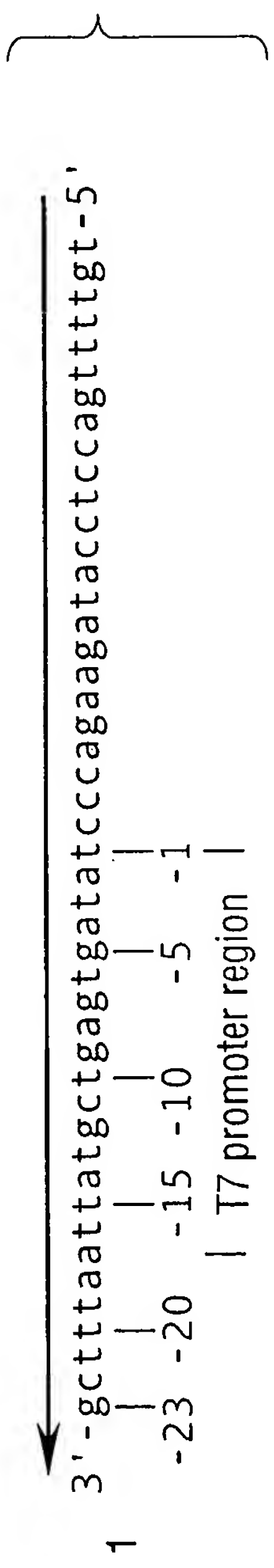


FIG. 93B

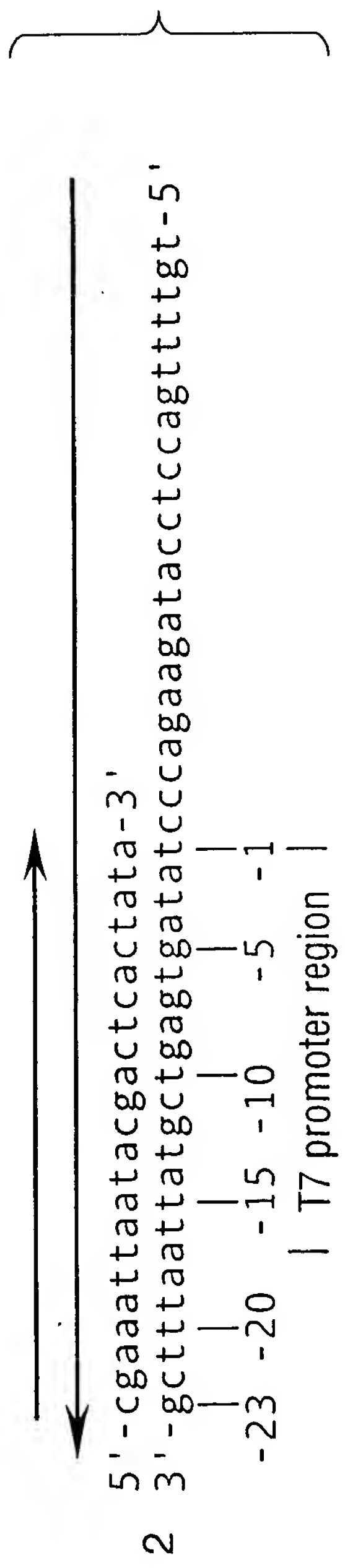
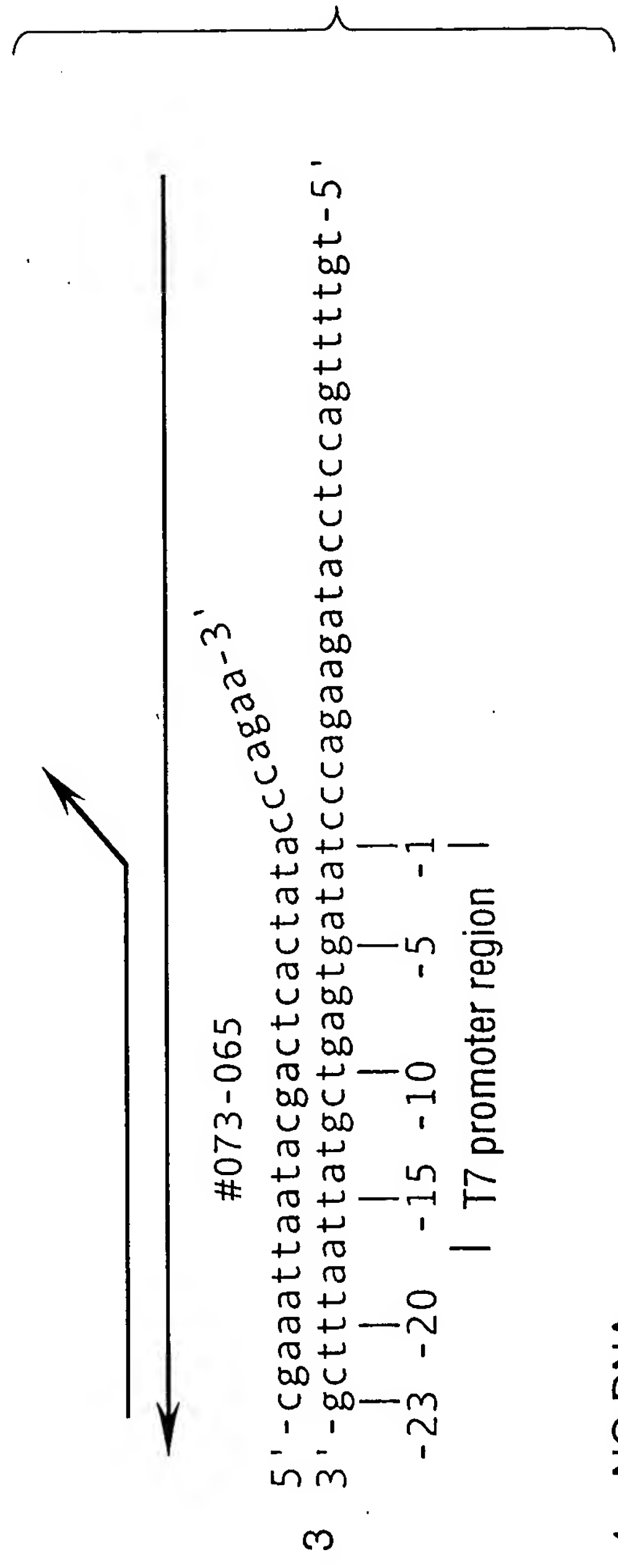


FIG. 93C



4 NO DNA

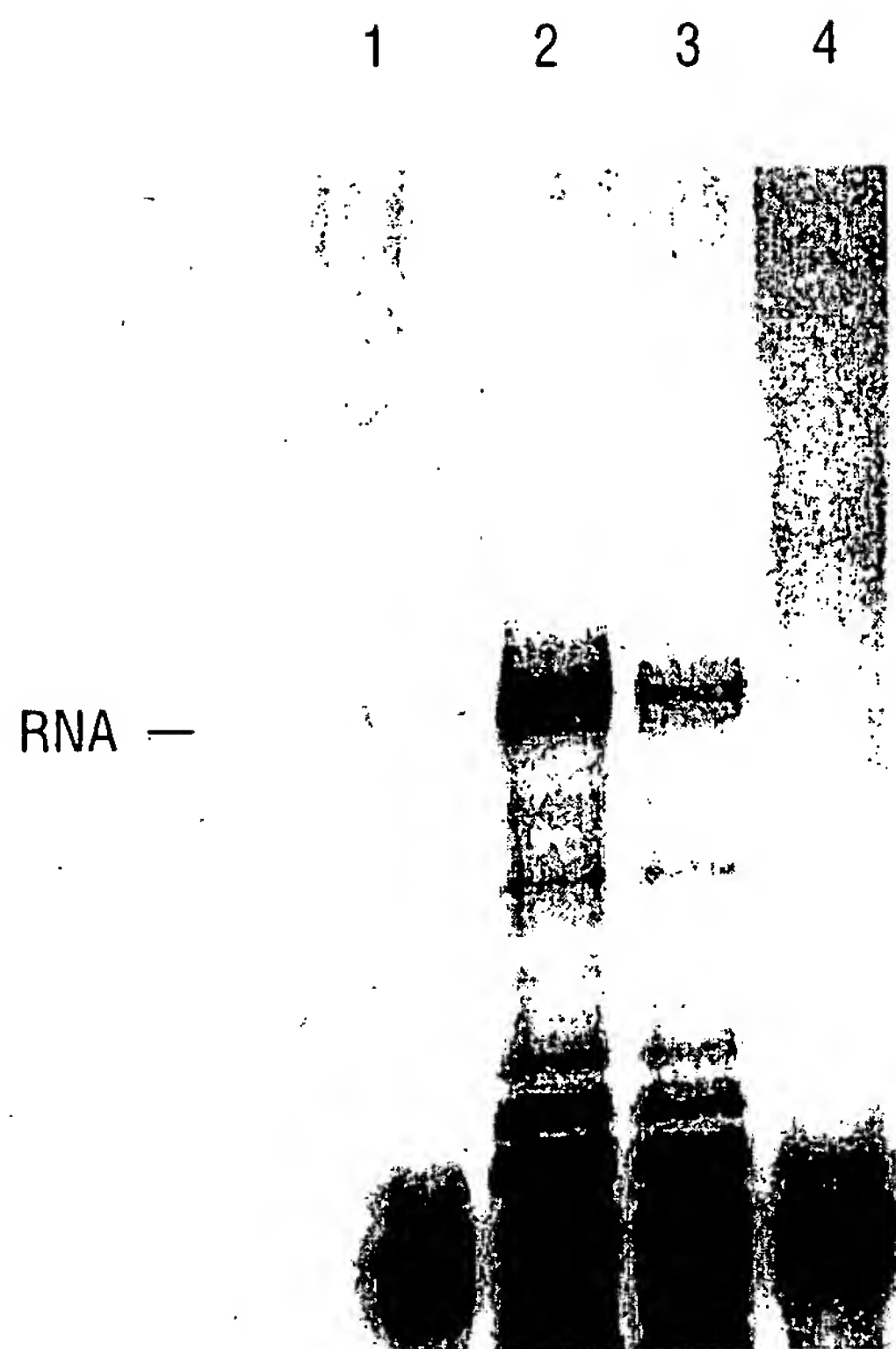
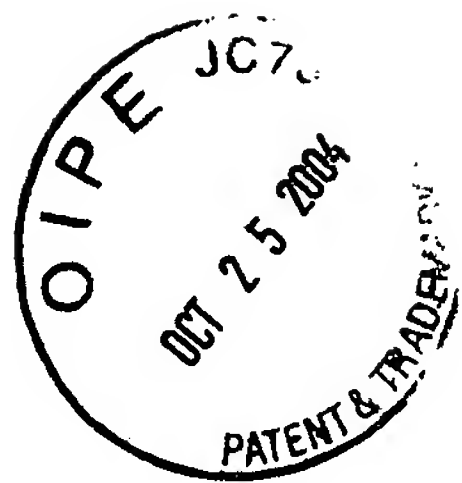


FIG. 93D

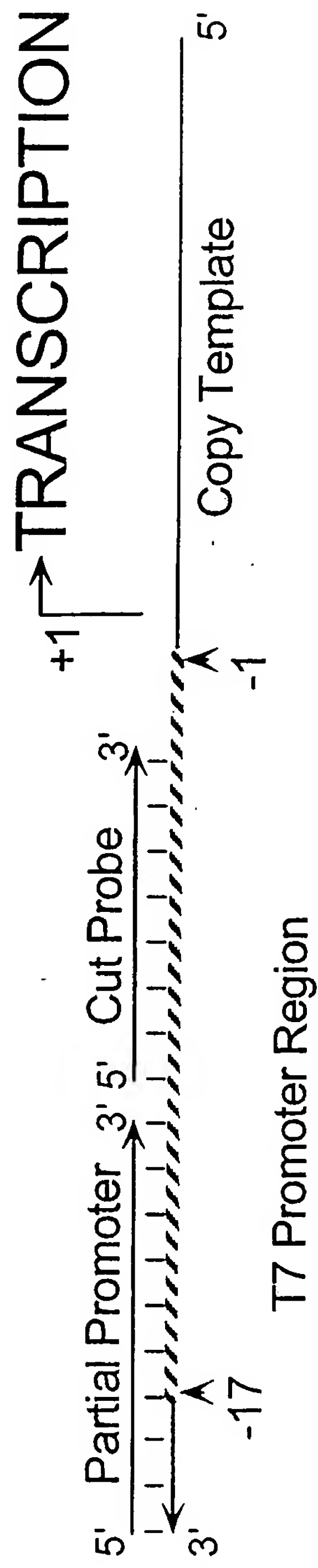
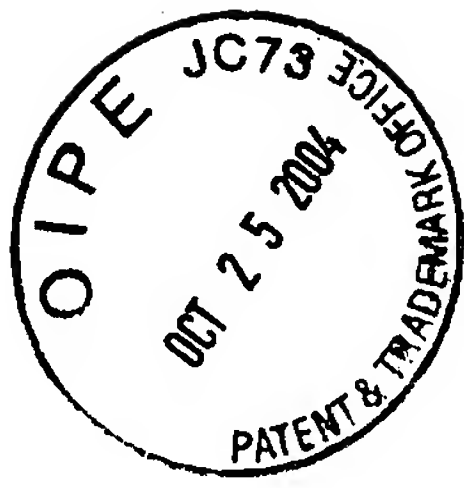
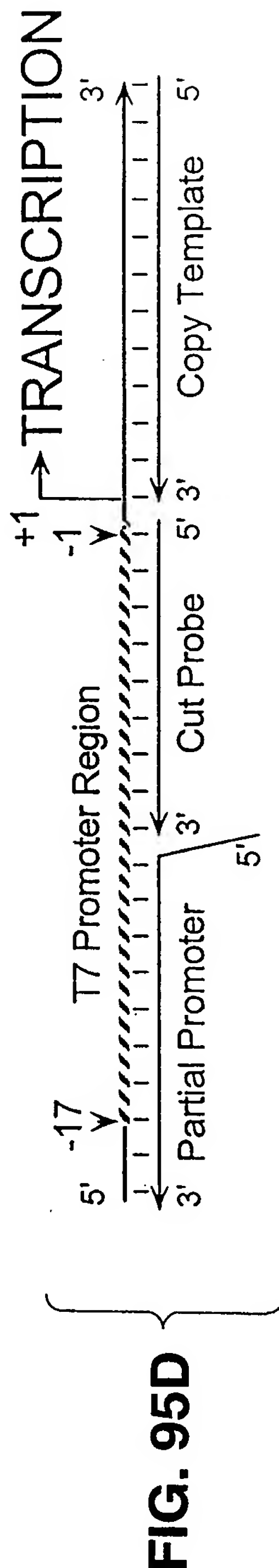
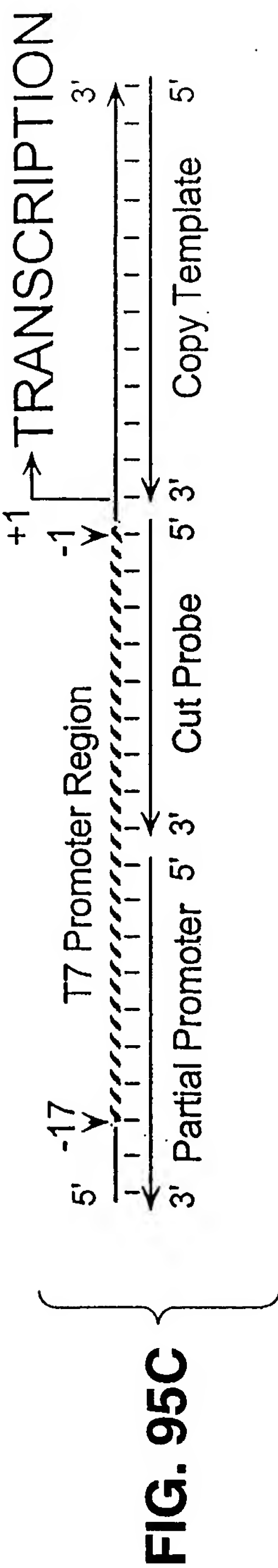
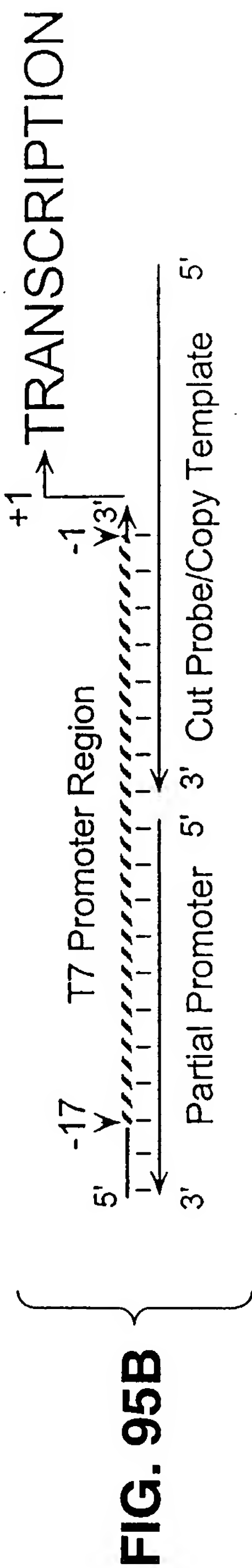
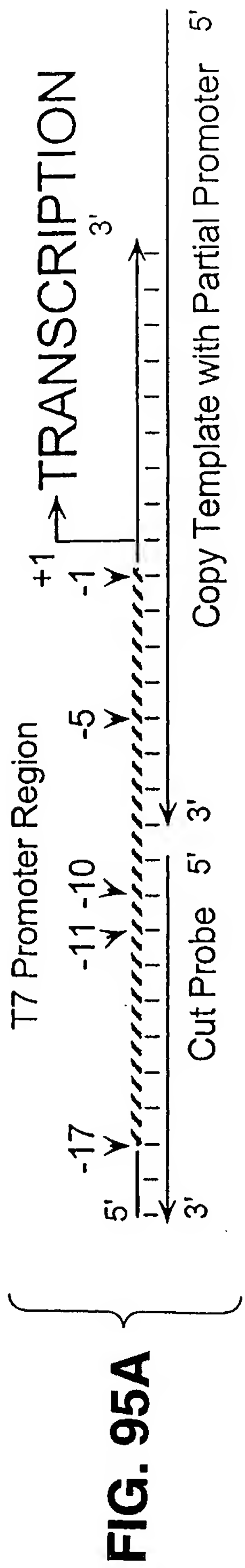


FIG. 94



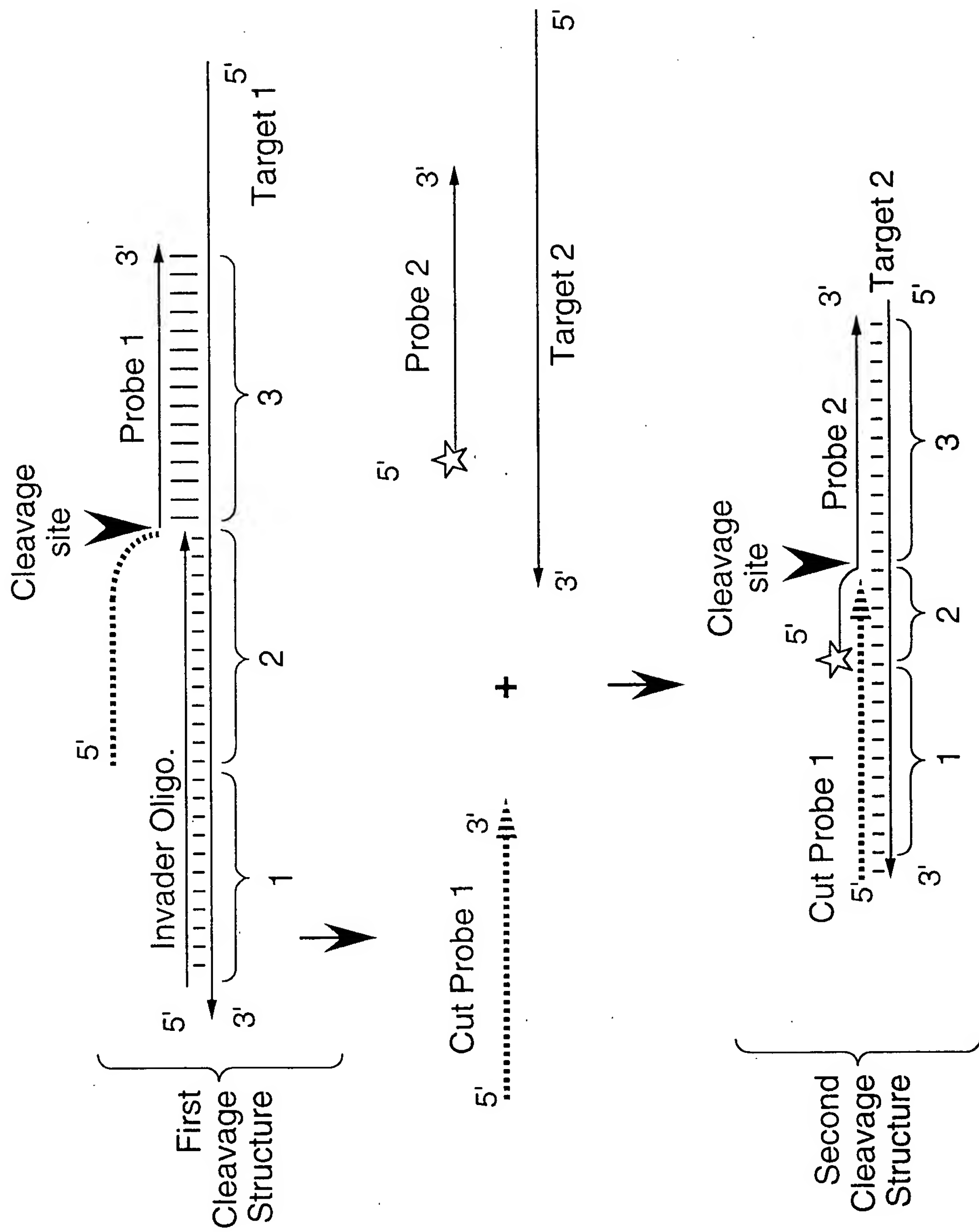


FIG. 96

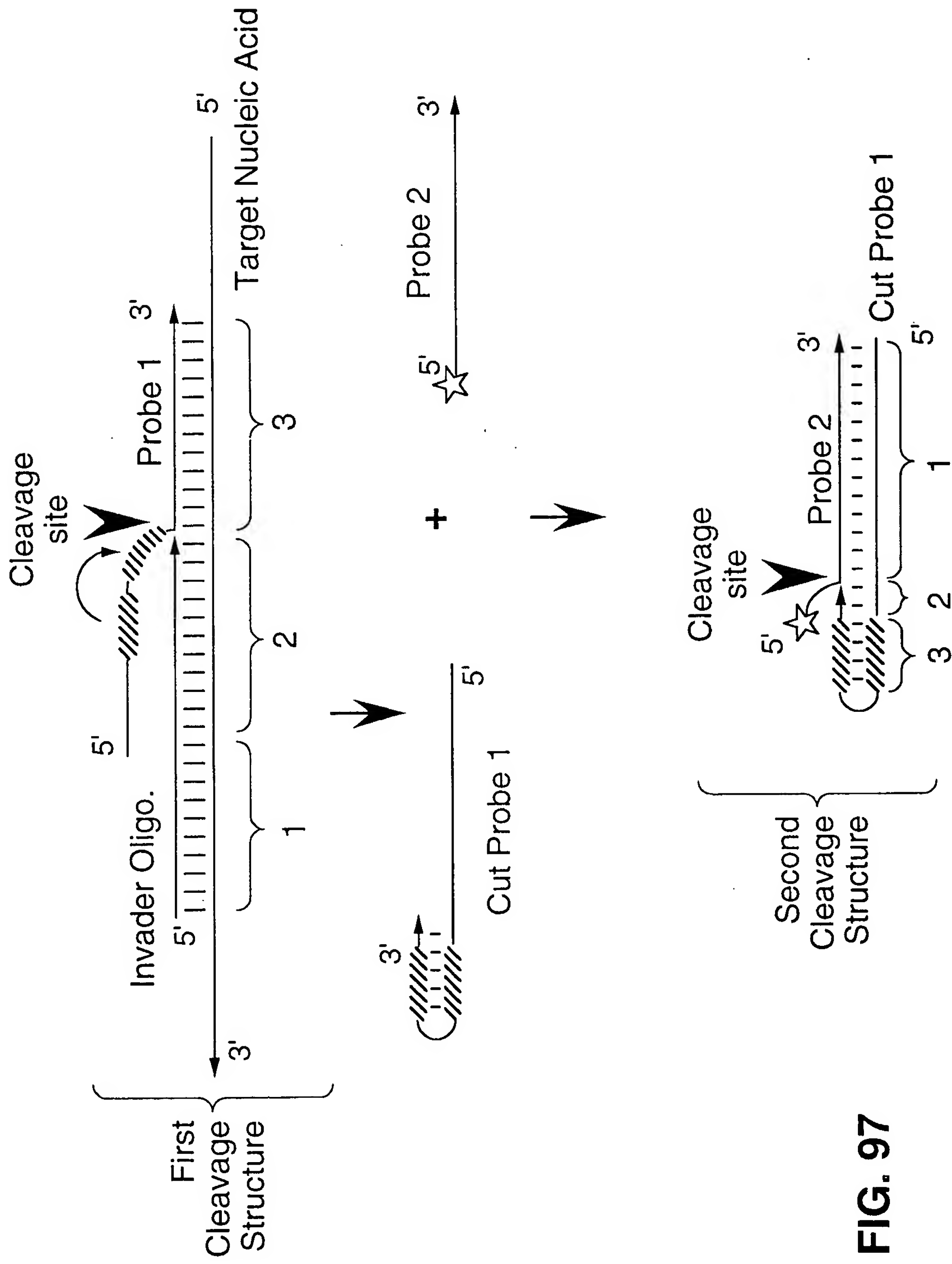
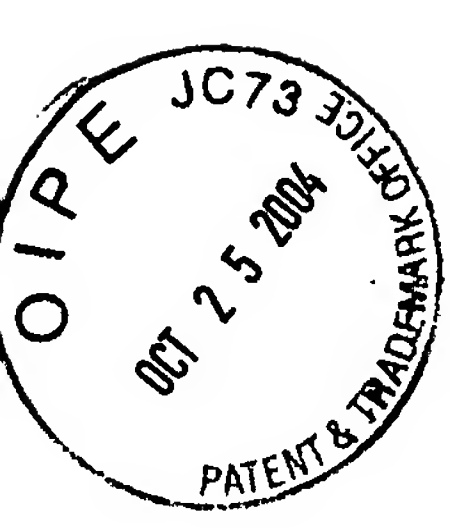


FIG. 97



PR1 probe

Cleavage site
↓
5'FITTTTCCAGAGCCTAAT G3'

IT3 Invader-Target

A^A ACGAGCGTCTTT G3'
G TGCTCGCAGAAAGGTCTCGGATTAATTTTTTTTTT5'

IT3-8 Invader-Target

A^A AGCGTCTT G3'
G TCGCAGAAGGTCTCGGATTAATTTTTTTTTT5'

IT3-6 Invader-Target

A^A CGTCTT G3'
G GCAGAAGGTCTCGGATTAATTTTTTTTTT5'

IT3-4 Invader-Target

A^A TCCTT G3'
G AGAAGGTCTCGGATTAATTTTTTTTTT5'

IT3-3 Invader-Target

A^A CTT G3'
G GAAGGTCTCGGATTAATTTTTTTTTT5'

IT3-0 Invader-Target

3'GAAGGTCTCGGATTAATTTTTTTTTT5'

FIG. 98

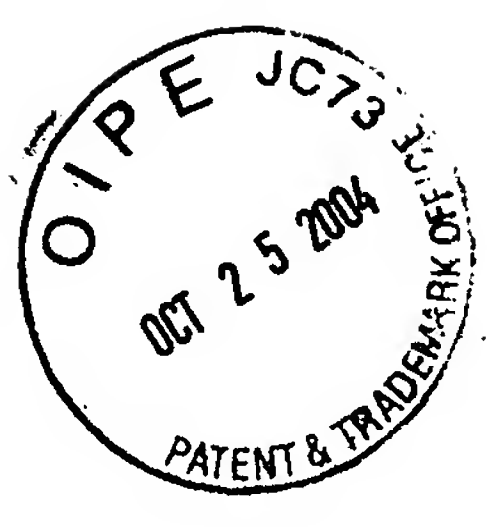


FIG. 99A

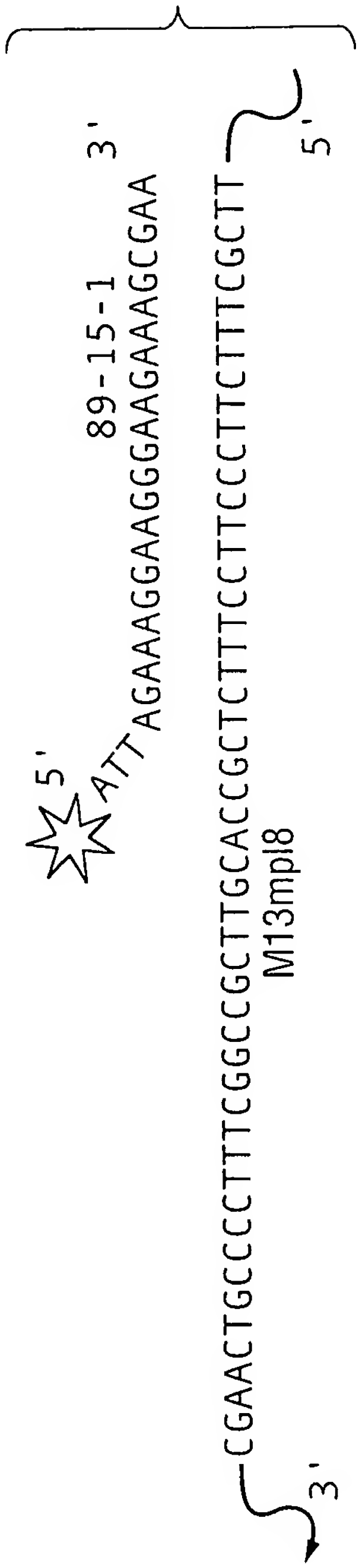


FIG. 99B

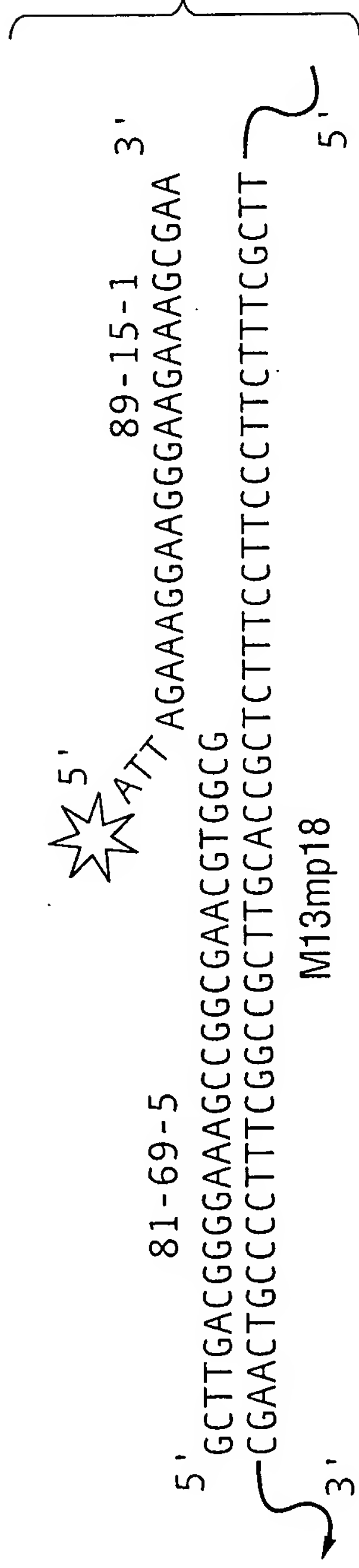
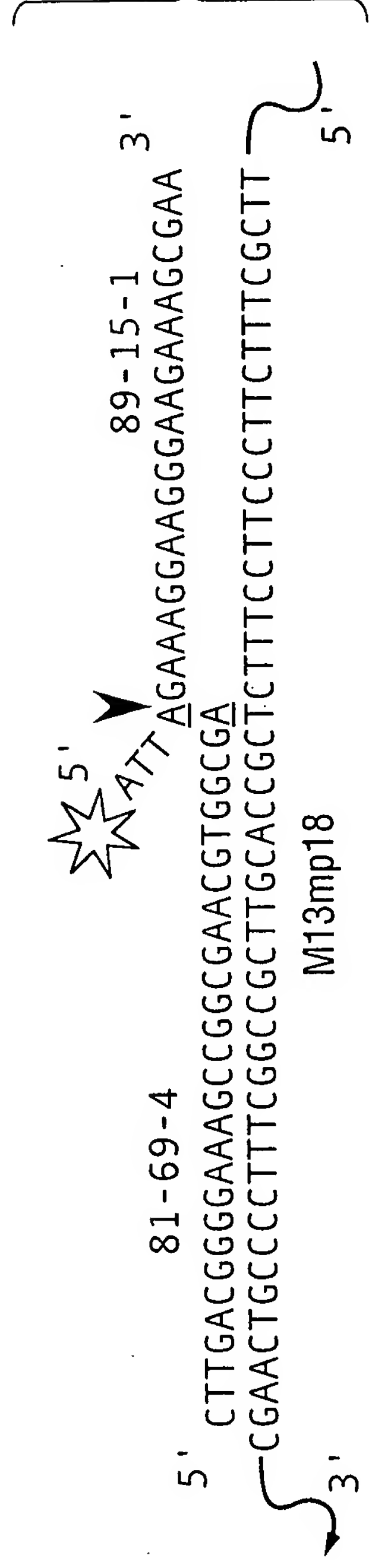
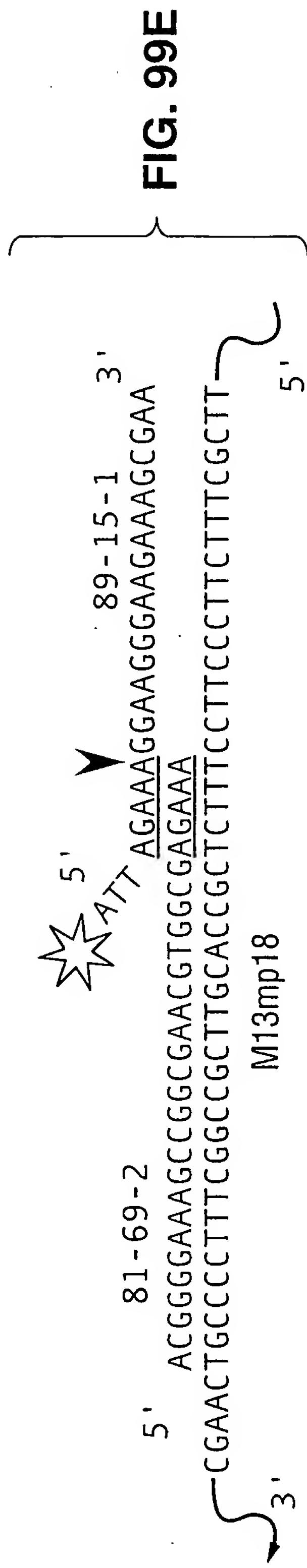
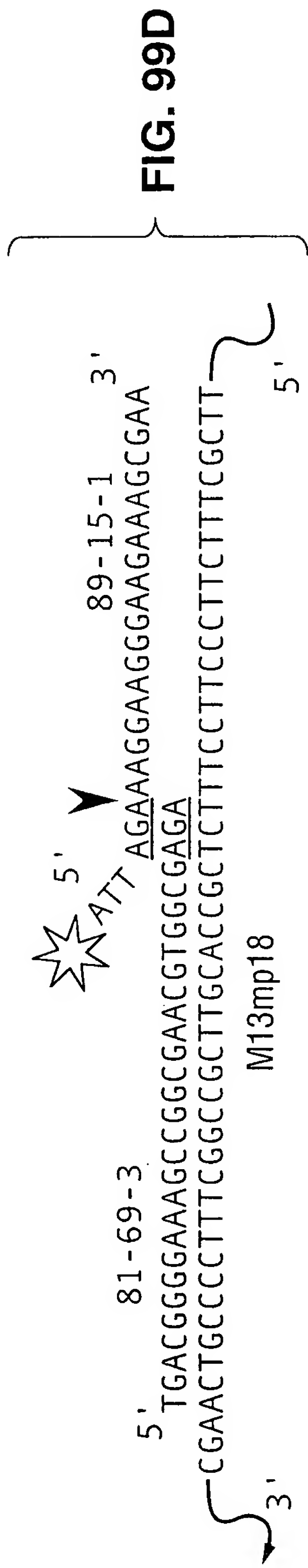


FIG. 99C





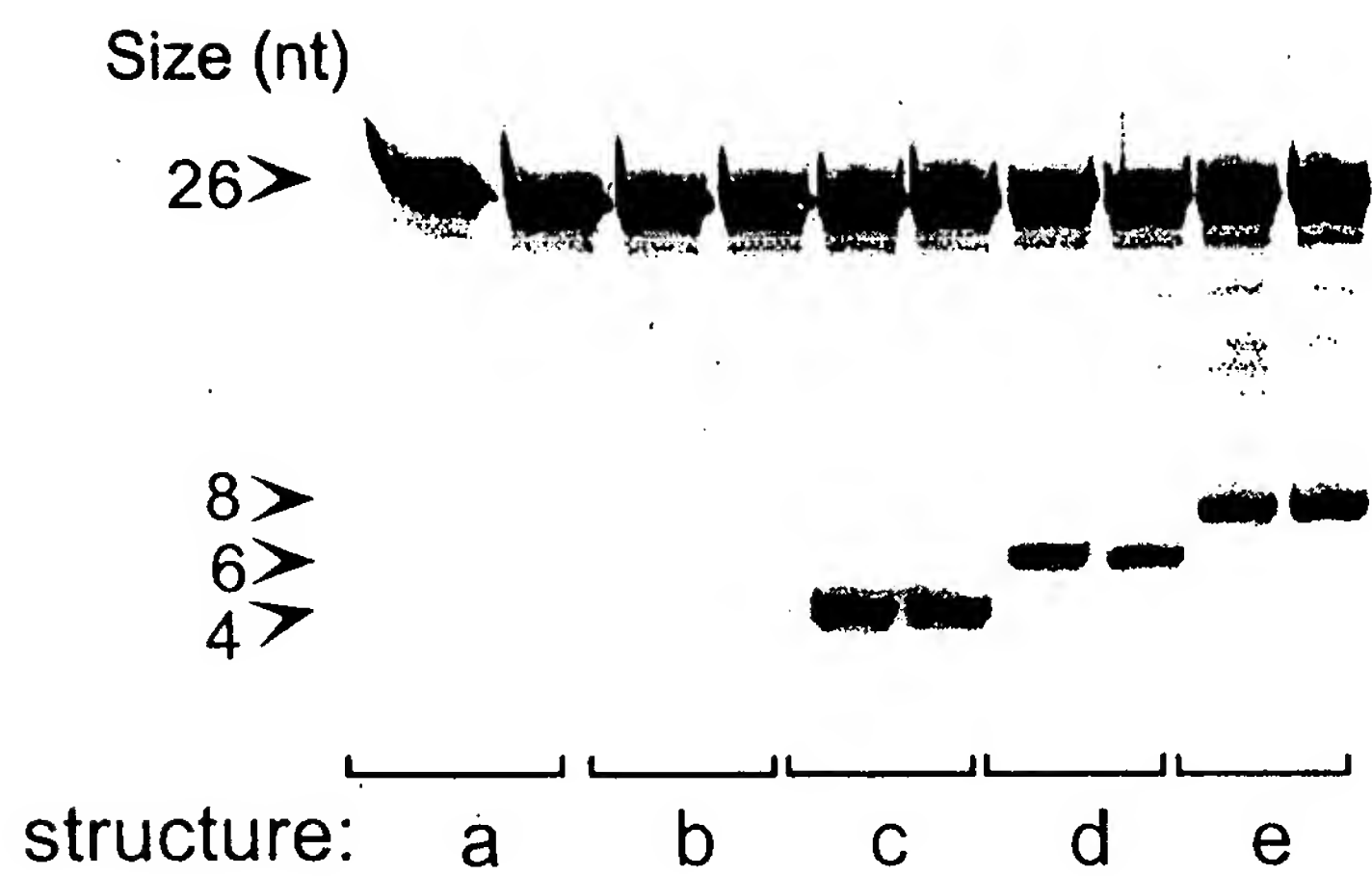
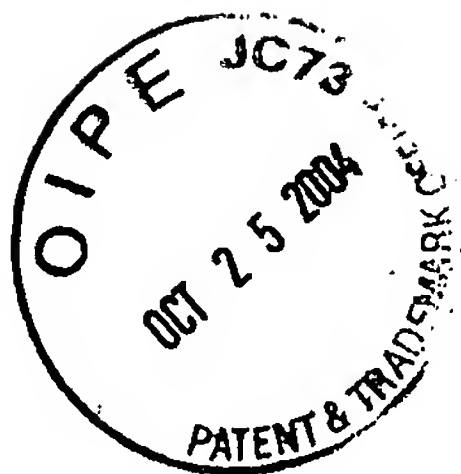


FIG. 100

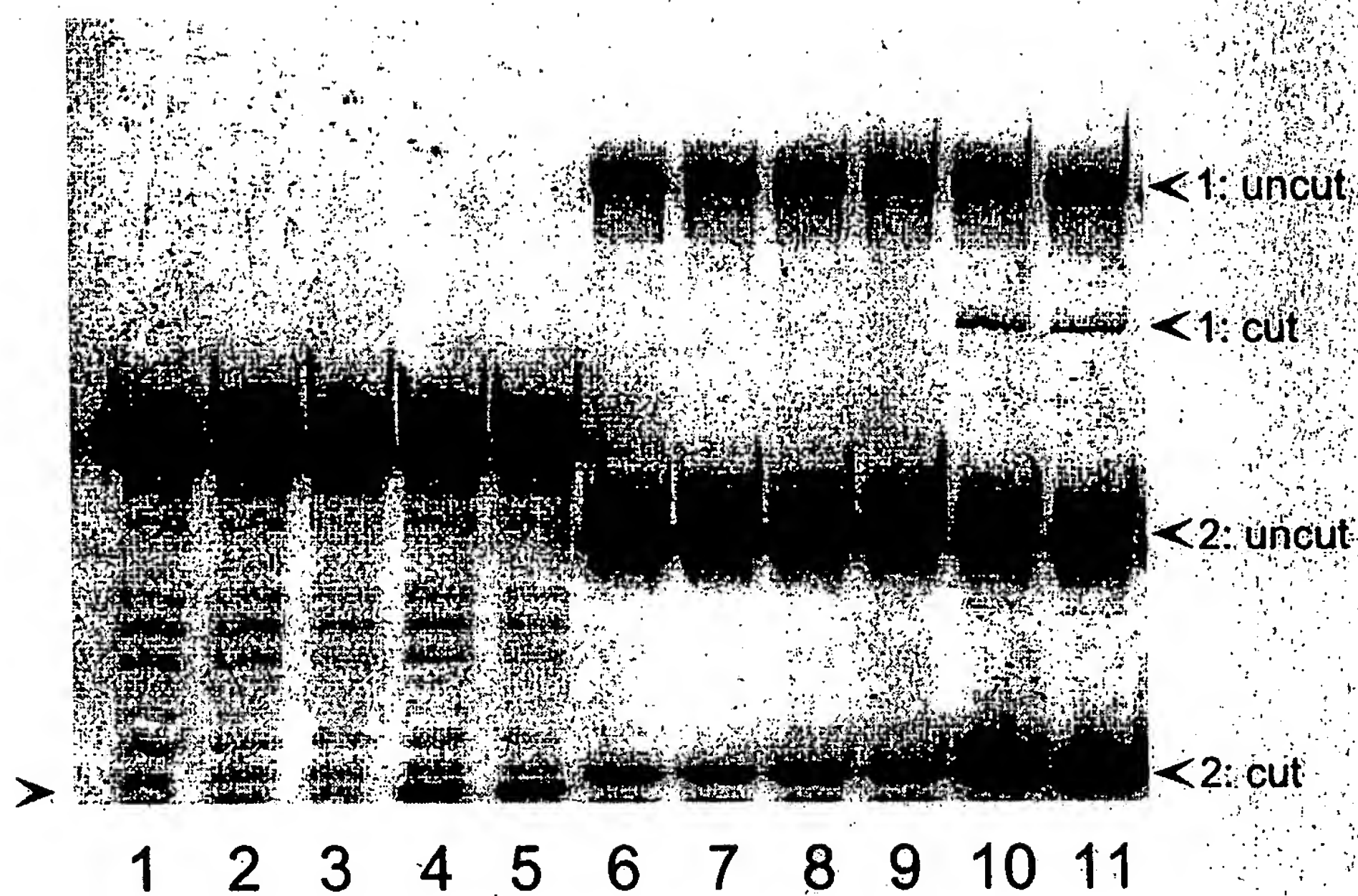
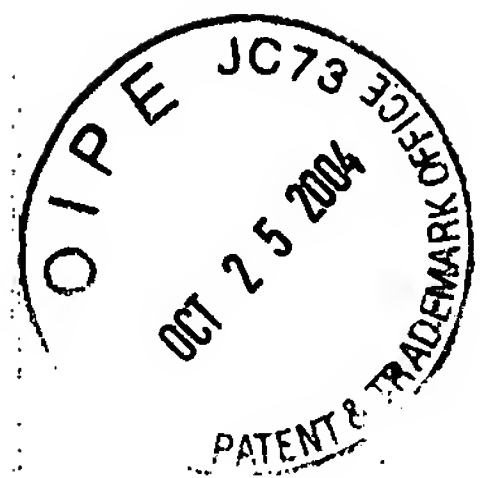
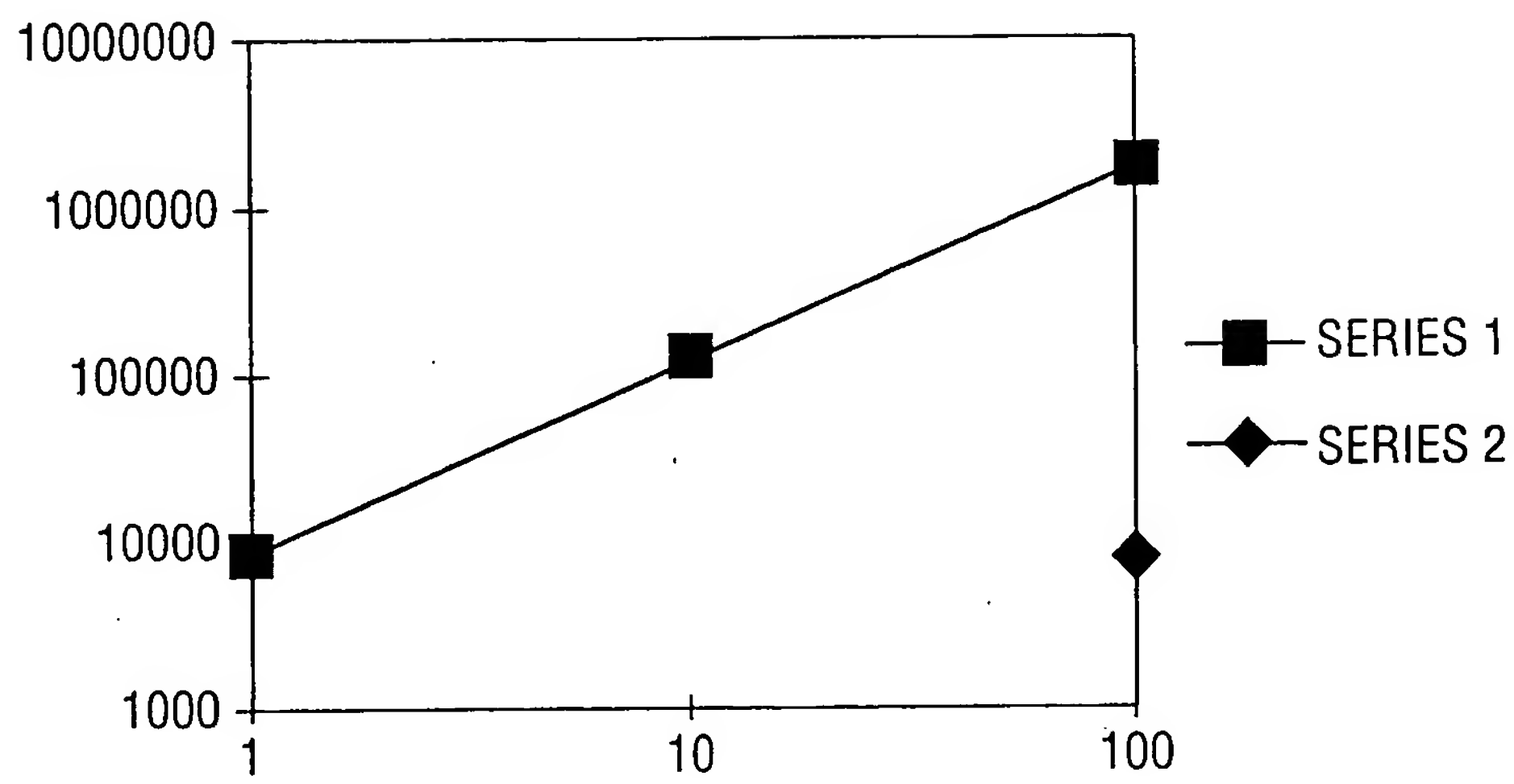
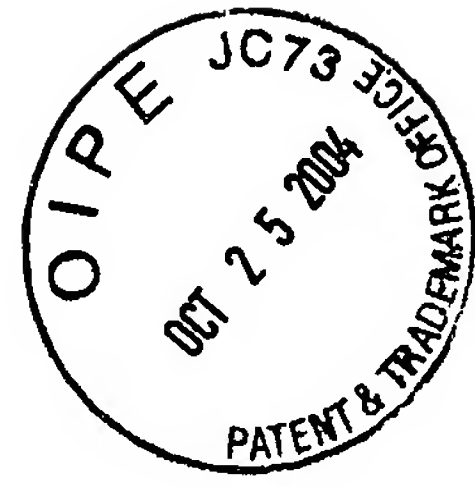


FIG. 101A



| | | |
|------------------|---------------|--------------|
| attomoles/target | basic invader | invader sqrd |
| 1 | | 8386 |
| 10 | | 133185 |
| 100 | 8512 | 1862211 |

FIG. 101B

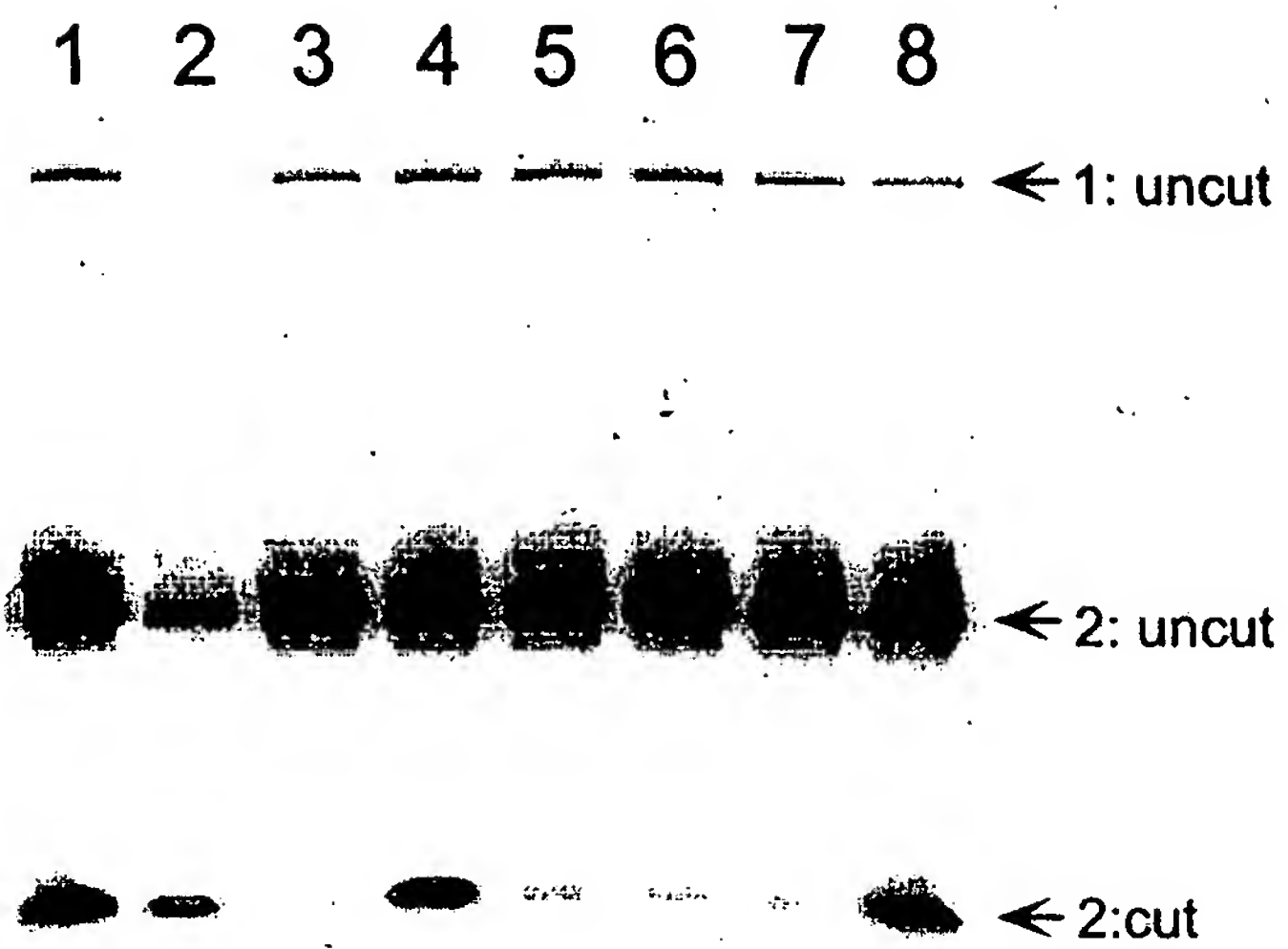
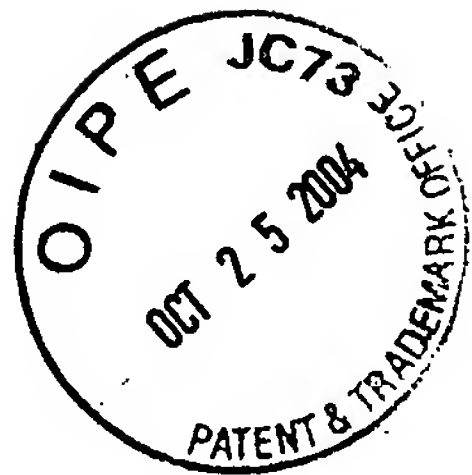


FIG. 102

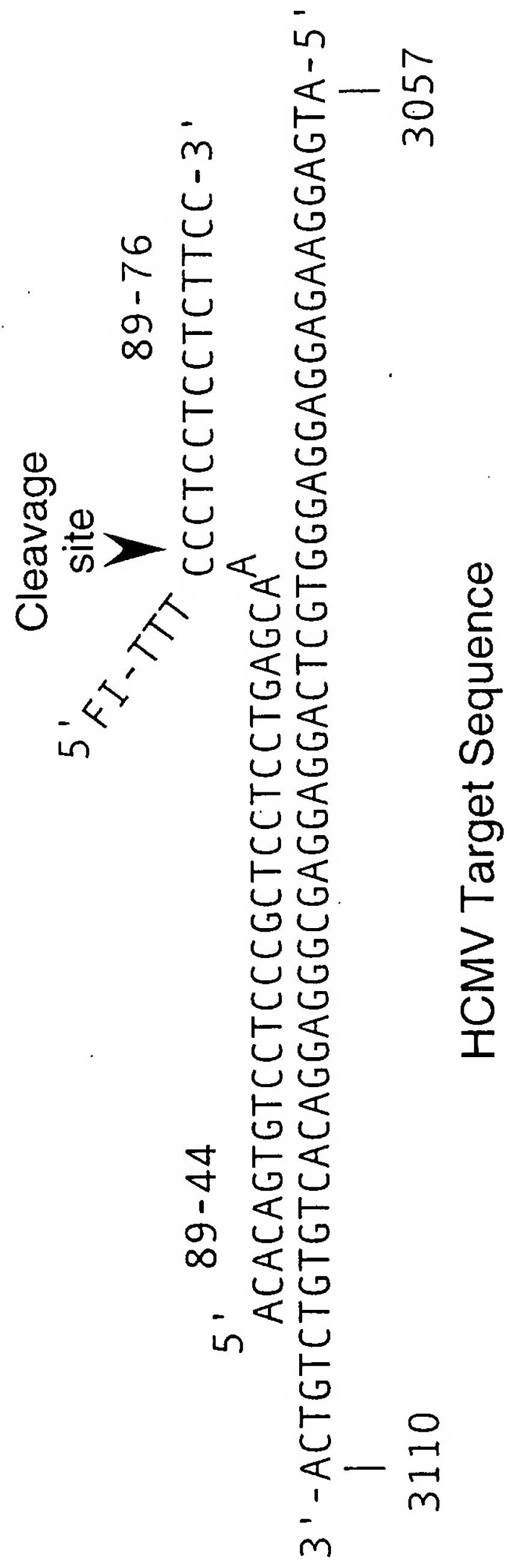
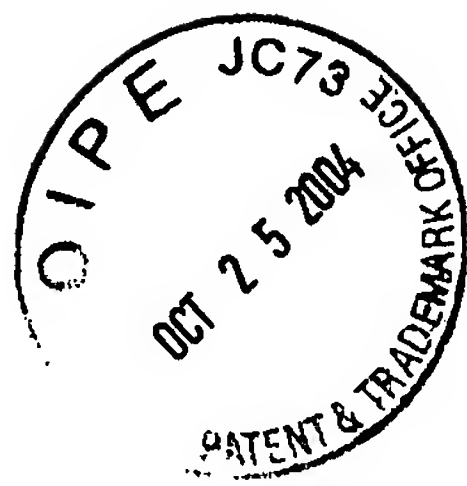


FIG. 103

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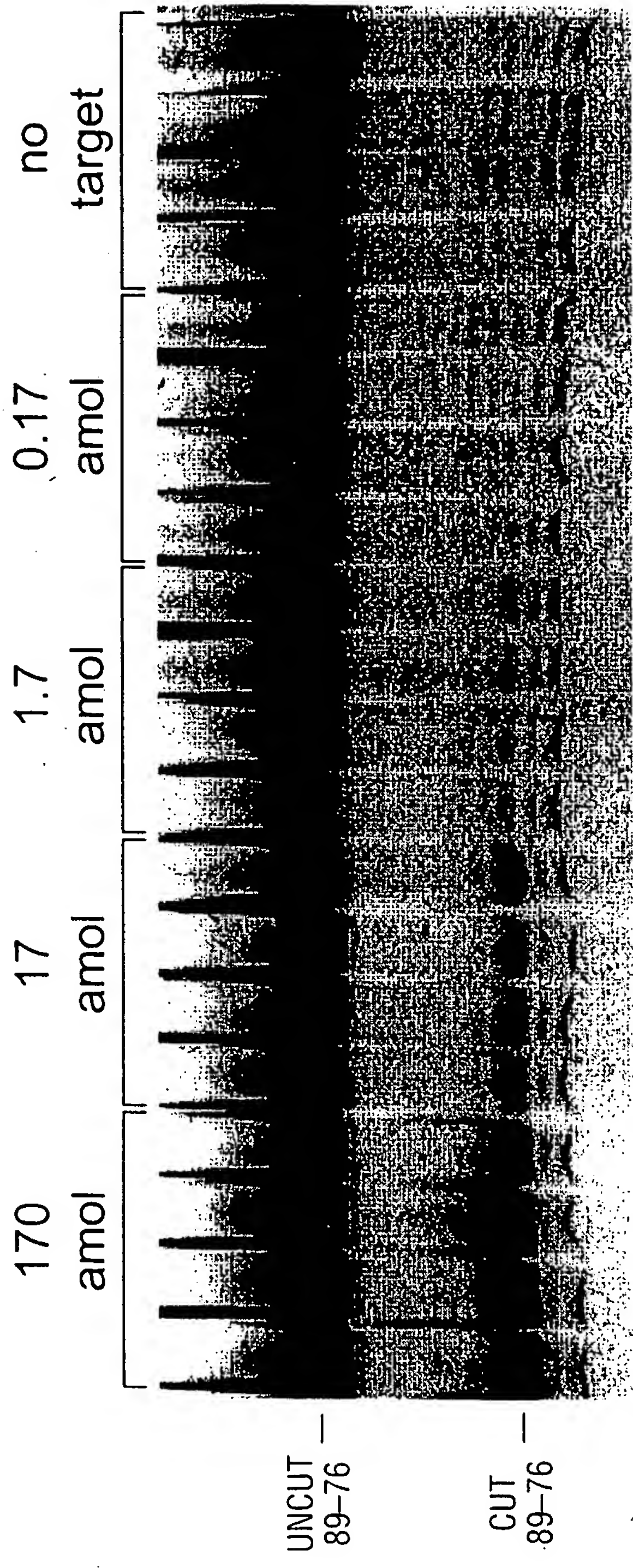


FIG. 104

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